

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 14:48:45 ; Search time 3856 Seconds
(without alignments)
10078.082 Million cell updates/sec

Title: US-10-074-246-65
Perfect score: 802
Sequence: 1 tcatagcaggcctcctcttg.....tggctgcgtacttcgccagc 802

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 19

Total number of hits satisfying chosen parameters: 197

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|-------------|--------------------|
| 1 | 802 | 100.0 | 802 | 6 | AX513136 | AX513136 Sequence |
| 2 | 802 | 100.0 | 327650 | 1 | BX248337 | BX248337 Mycobacte |
| 3 | 802 | 100.0 | 349306 | 1 | BX842575 | BX842575 Mycobacte |
| 4 | 751 | 93.6 | 110000 | 1 | AE000516_10 | Continuation (11 o |

| | | | | | | | |
|----|-----|------|--------|---|----------|----------|-------------|
| 5 | 577 | 71.9 | 628 | 6 | AX513137 | AX513137 | Sequence |
| 6 | 369 | 46.0 | 369 | 6 | BD171700 | BD171700 | Identific |
| 7 | 302 | 37.7 | 323 | 6 | BD171699 | BD171699 | Identific |
| 8 | 196 | 24.4 | 1058 | 6 | AR169193 | AR169193 | Sequence |
| 9 | 196 | 24.4 | 1058 | 6 | BD205858 | BD205858 | Compounds |
| 10 | 196 | 24.4 | 1058 | 6 | CQ785444 | CQ785444 | Sequence |
| 11 | 196 | 24.4 | 1058 | 6 | AR182483 | AR182483 | Sequence |
| 12 | 196 | 24.4 | 1058 | 6 | AR194866 | AR194866 | Sequence |
| 13 | 196 | 24.4 | 1058 | 6 | AR233138 | AR233138 | Sequence |
| 14 | 196 | 24.4 | 1058 | 6 | AR353343 | AR353343 | Sequence |
| 15 | 196 | 24.4 | 1058 | 6 | AX429637 | AX429637 | Sequence |
| 16 | 196 | 24.4 | 1058 | 6 | AX832622 | AX832622 | Sequence |
| 17 | 196 | 24.4 | 1058 | 6 | BD006366 | BD006366 | Compounds |
| 18 | 196 | 24.4 | 1058 | 6 | BD006486 | BD006486 | Compounds |
| 19 | 196 | 24.4 | 1058 | 6 | BD069326 | BD069326 | Compounds |
| 20 | 194 | 24.2 | 611 | 6 | BD171688 | BD171688 | Identific |
| 21 | 159 | 19.8 | 611 | 6 | BD171689 | BD171689 | Identific |
| 22 | 46 | 5.7 | 712 | 6 | AX513135 | AX513135 | Sequence |
| 23 | 31 | 3.9 | 745 | 6 | AX513131 | AX513131 | Sequence |
| 24 | 30 | 3.7 | 594 | 6 | BD171693 | BD171693 | Identific |
| 25 | 30 | 3.7 | 785 | 6 | AX513132 | AX513132 | Sequence |
| 26 | 29 | 3.6 | 625 | 6 | BD171692 | BD171692 | Identific |
| 27 | 29 | 3.6 | 642 | 6 | AX513130 | AX513130 | Sequence |
| 28 | 26 | 3.2 | 533 | 6 | BD171695 | BD171695 | Identific |
| 29 | 26 | 3.2 | 690 | 6 | BD171684 | BD171684 | Identific |
| 30 | 26 | 3.2 | 690 | 6 | BD171685 | BD171685 | Identific |
| 31 | 26 | 3.2 | 691 | 6 | AX513133 | AX513133 | Sequence |
| 32 | 26 | 3.2 | 698 | 6 | AX513134 | AX513134 | Sequence |
| 33 | 26 | 3.2 | 707 | 6 | AX513139 | AX513139 | Sequence |
| 34 | 26 | 3.2 | 724 | 6 | BD171686 | BD171686 | Identific |
| 35 | 26 | 3.2 | 731 | 6 | BD171687 | BD171687 | Identific |
| 36 | 26 | 3.2 | 881 | 6 | AX513129 | AX513129 | Sequence |
| 37 | 26 | 3.2 | 1832 | 1 | MP34KDA | X68102 | Mycobacteri |
| 38 | 26 | 3.2 | 1839 | 6 | A28087 | A28087 | M.paratuber |
| 39 | 26 | 3.2 | 1839 | 6 | AR209771 | AR209771 | Sequence |
| 40 | 26 | 3.2 | 3200 | 1 | AF411607 | AF411607 | Mycobacte |
| 41 | 26 | 3.2 | 303855 | 1 | AE017230 | AE017230 | Mycobacte |
| 42 | 24 | 3.0 | 24 | 6 | AX513119 | AX513119 | Sequence |
| 43 | 24 | 3.0 | 551 | 6 | BD171694 | BD171694 | Identific |
| 44 | 24 | 3.0 | 668 | 6 | BD171691 | BD171691 | Identific |
| 45 | 24 | 3.0 | 669 | 6 | BD171690 | BD171690 | Identific |

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 14:16:30 ; Search time 561 Seconds
(without alignments)
8462.803 Million cell updates/sec

Title: US-10-074-246-65
Perfect score: 802
Sequence: 1 tcatagcaggcctcctcttg.....tggctgcgtacttcgccagc 802

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 19

Total number of hits satisfying chosen parameters: 117

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|------------------|--------|----|-------------|--------------------|
| 1 | 802 | 100.0 | 802 | 6 | ABS70084 | Abs70084 Mycobacte |
| 2 | 802 | 100.0 | 802 | 8 | ABX10110 | Abx10110 M. tuberc |
| 3 | 802 | 100.0 | 110000 | 4 | AAI99682_10 | Continuation (11 o |
| 4 | 751 | 93.6 | 110000 | 4 | AAI99683_10 | Continuation (11 o |
| 5 | 648 | 80.8 | 648 | 8 | ABX10126 | Abx10126 M. tuberc |

| | | | | | | |
|----|-----|------|------|---|----------|--------------------|
| 6 | 579 | 72.2 | 648 | 8 | ABX10127 | Abx10127 M. bovis |
| 7 | 577 | 71.9 | 628 | 6 | ABS70085 | Abs70085 Mycobacte |
| 8 | 577 | 71.9 | 628 | 8 | ABX10111 | Abx10111 M. bovis |
| 9 | 196 | 24.4 | 1058 | 2 | AAT91444 | Aat91444 Mycobacte |
| 10 | 196 | 24.4 | 1058 | 2 | AAT91508 | Aat91508 Mycobacte |
| 11 | 196 | 24.4 | 1058 | 2 | AAV44383 | Aav44383 Mycobacte |
| 12 | 196 | 24.4 | 1058 | 2 | AAV64491 | Aav64491 M. tuberc |
| 13 | 196 | 24.4 | 1058 | 2 | AAZ19081 | Aaz19081 M. tuberc |
| 14 | 196 | 24.4 | 1058 | 2 | AAZ19293 | Aaz19293 M. tuberc |
| 15 | 46 | 5.7 | 712 | 6 | ABS70083 | Abs70083 Mycobacte |
| 16 | 46 | 5.7 | 712 | 8 | ABX10109 | Abx10109 M. szulga |
| 17 | 31 | 3.9 | 570 | 8 | ABX10133 | Abx10133 M. szulga |
| 18 | 31 | 3.9 | 588 | 8 | ABX10132 | Abx10132 M. gordon |
| 19 | 31 | 3.9 | 745 | 6 | ABS70079 | Abs70079 Mycobacte |
| 20 | 31 | 3.9 | 745 | 8 | ABX10107 | Abx10107 M. malmoe |
| 21 | 31 | 3.9 | 881 | 8 | ABX10113 | Abx10113 M. avium |
| 22 | 30 | 3.7 | 662 | 8 | ABX10130 | Abx10130 M. gastri |
| 23 | 30 | 3.7 | 785 | 6 | ABS70080 | Abs70080 Mycobacte |
| 24 | 30 | 3.7 | 785 | 8 | ABX10104 | Abx10104 M. gordon |
| 25 | 29 | 3.6 | 631 | 8 | ABX10131 | Abx10131 M. kansas |
| 26 | 29 | 3.6 | 642 | 6 | ABS70078 | Abs70078 Mycobacte |
| 27 | 29 | 3.6 | 642 | 8 | ABX10106 | Abx10106 M. kansas |
| 28 | 29 | 3.6 | 705 | 8 | ABX10129 | Abx10129 M. ulcera |
| 29 | 29 | 3.6 | 706 | 8 | ABX10128 | Abx10128 M. marinu |
| 30 | 28 | 3.5 | 768 | 8 | ABX10125 | Abx10125 M. simae |
| 31 | 26 | 3.2 | 691 | 6 | ABS70081 | Abs70081 Mycobacte |
| 32 | 26 | 3.2 | 698 | 6 | ABS70082 | Abs70082 Mycobacte |
| 33 | 26 | 3.2 | 707 | 6 | ABS70087 | Abs70087 Mycobacte |
| 34 | 26 | 3.2 | 707 | 8 | ABX10114 | Abx10114 M. paratu |
| 35 | 26 | 3.2 | 727 | 8 | ABX10123 | Abx10123 M. paratu |
| 36 | 26 | 3.2 | 727 | 8 | ABX10122 | Abx10122 M. avium |
| 37 | 26 | 3.2 | 741 | 8 | ABX10105 | Abx10105 M. intrac |
| 38 | 26 | 3.2 | 748 | 8 | ABX10108 | Abx10108 M. simae |
| 39 | 26 | 3.2 | 761 | 8 | ABX10124 | Abx10124 M. malmoe |
| 40 | 26 | 3.2 | 881 | 6 | ABS70077 | Abs70077 Mycobacte |
| 41 | 26 | 3.2 | 1839 | 2 | AAQ29147 | Aaq29147 DNA encod |
| 42 | 24 | 3.0 | 24 | 6 | ABS70067 | Abs70067 Mycobacte |
| 43 | 24 | 3.0 | 685 | 6 | ABS70089 | Abs70089 Mycobacte |
| 44 | 24 | 3.0 | 685 | 8 | ABX10116 | Abx10116 M. ulcera |
| 45 | 24 | 3.0 | 686 | 6 | ABS70088 | Abs70088 Mycobacte |

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 18:32:59 ; Search time 185 Seconds
(without alignments)
7093.481 Million cell updates/sec

Title: US-10-074-246-65
Perfect score: 802
Sequence: 1 tcatagcaggcctcctcttg.....tggctgcgtacttcgccagc 802

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 19

Total number of hits satisfying chosen parameters: 34

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | | % | | Query | | DB | ID | Description |
|--------|-----|-------|-------|---------|-------|--------------------|----|----|-------------------|
| | No. | Score | Match | Length | | | | | |
| | 1 | 802 | 100.0 | 4411529 | 3 | US-09-103-840A-1 | | | Sequence 1, Appli |
| | 2 | 751 | 93.6 | 4403765 | 3 | US-09-103-840A-2 | | | Sequence 2, Appli |
| | 3 | 196 | 24.4 | 1058 | 3 | US-08-818-112-45 | | | Sequence 45, Appl |
| | 4 | 196 | 24.4 | 1058 | 3 | US-08-818-111-45 | | | Sequence 45, Appl |
| | 5 | 196 | 24.4 | 1058 | 3 | US-09-056-556-45 | | | Sequence 45, Appl |
| | 6 | 196 | 24.4 | 1058 | 3 | US-09-072-596-45 | | | Sequence 45, Appl |
| | 7 | 196 | 24.4 | 1058 | 4 | US-09-072-967-45 | | | Sequence 45, Appl |
| | 8 | 26 | 3.2 | 1839 | 3 | US-08-122-458D-10 | | | Sequence 10, Appl |
| | 9 | 20 | 2.5 | 1983 | 4 | US-09-902-540-3373 | | | Sequence 3373, Ap |
| c | 10 | 20 | 2.5 | 17125 | 4 | US-09-902-540-1158 | | | Sequence 1158, Ap |
| | 11 | 19 | 2.4 | 717 | 3 | US-09-124-238A-7 | | | Sequence 7, Appli |
| | 12 | 19 | 2.4 | 717 | 3 | US-09-721-975-7 | | | Sequence 7, Appli |

| | | | | | | | |
|---|----|----|-----|-------|---|---------------------|-------------------|
| | 13 | 19 | 2.4 | 717 | 4 | US-09-986-621-7 | Sequence 7, Appli |
| | 14 | 19 | 2.4 | 765 | 3 | US-09-124-238A-21 | Sequence 21, Appl |
| | 15 | 19 | 2.4 | 765 | 3 | US-09-721-975-21 | Sequence 21, Appl |
| | 16 | 19 | 2.4 | 765 | 4 | US-09-986-621-21 | Sequence 21, Appl |
| | 17 | 19 | 2.4 | 1488 | 3 | US-09-124-238A-8 | Sequence 8, Appli |
| | 18 | 19 | 2.4 | 1488 | 3 | US-09-721-975-8 | Sequence 8, Appli |
| | 19 | 19 | 2.4 | 1488 | 4 | US-09-986-621-8 | Sequence 8, Appli |
| c | 20 | 19 | 2.4 | 1589 | 4 | US-09-634-238-68 | Sequence 68, Appl |
| | 21 | 19 | 2.4 | 1620 | 3 | US-09-124-238A-32 | Sequence 32, Appl |
| | 22 | 19 | 2.4 | 1620 | 3 | US-09-721-975-32 | Sequence 32, Appl |
| | 23 | 19 | 2.4 | 1620 | 4 | US-09-986-621-32 | Sequence 32, Appl |
| | 24 | 19 | 2.4 | 1644 | 3 | US-09-124-238A-9 | Sequence 9, Appli |
| | 25 | 19 | 2.4 | 1644 | 3 | US-09-721-975-9 | Sequence 9, Appli |
| | 26 | 19 | 2.4 | 1644 | 4 | US-09-986-621-9 | Sequence 9, Appli |
| | 27 | 19 | 2.4 | 1665 | 3 | US-09-124-238A-33 | Sequence 33, Appl |
| | 28 | 19 | 2.4 | 1665 | 3 | US-09-721-975-33 | Sequence 33, Appl |
| | 29 | 19 | 2.4 | 1665 | 4 | US-09-986-621-33 | Sequence 33, Appl |
| | 30 | 19 | 2.4 | 1689 | 3 | US-09-124-238A-22 | Sequence 22, Appl |
| | 31 | 19 | 2.4 | 1689 | 3 | US-09-721-975-22 | Sequence 22, Appl |
| | 32 | 19 | 2.4 | 1689 | 4 | US-09-986-621-22 | Sequence 22, Appl |
| | 33 | 19 | 2.4 | 1690 | 4 | US-09-949-016-3384 | Sequence 3384, Ap |
| | 34 | 19 | 2.4 | 18196 | 4 | US-09-949-016-15126 | Sequence 15126, A |

Run on: July 12, 2005, 19:19:37 ; Search time 643 Seconds
(without alignments)
7830.819 Million cell updates/sec

Title: US-10-074-246-65
Perfect score: 802
Sequence: 1 tcatagcaggcctcctcttg.....tggctgcgtacttcgccagc 802

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 6330945 seqs, 3139162390 residues

Word size : 19

Total number of hits satisfying chosen parameters: 82

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | % Query |
|--------|------------|
|--------|------------|

| No. | Score | Match | Length | DB | ID | Description |
|------|-------|-------|--------|----|----------------------|-------------------|
| 1 | 802 | 100.0 | 802 | 14 | US-10-074-246-65 | Sequence 65, Appl |
| 2 | 577 | 71.9 | 628 | 14 | US-10-074-246-66 | Sequence 66, Appl |
| 3 | 196 | 24.4 | 1058 | 15 | US-10-193-002-45 | Sequence 45, Appl |
| 4 | 196 | 24.4 | 1058 | 15 | US-10-084-843-45 | Sequence 45, Appl |
| 5 | 196 | 24.4 | 1058 | 24 | US-11-028-898-45 | Sequence 45, Appl |
| 6 | 46 | 5.7 | 712 | 14 | US-10-074-246-64 | Sequence 64, Appl |
| 7 | 31 | 3.9 | 745 | 14 | US-10-074-246-60 | Sequence 60, Appl |
| 8 | 30 | 3.7 | 785 | 14 | US-10-074-246-61 | Sequence 61, Appl |
| 9 | 29 | 3.6 | 642 | 14 | US-10-074-246-59 | Sequence 59, Appl |
| 10 | 26 | 3.2 | 691 | 14 | US-10-074-246-62 | Sequence 62, Appl |
| 11 | 26 | 3.2 | 698 | 14 | US-10-074-246-63 | Sequence 63, Appl |
| 12 | 26 | 3.2 | 707 | 14 | US-10-074-246-68 | Sequence 68, Appl |
| 13 | 26 | 3.2 | 881 | 14 | US-10-074-246-58 | Sequence 58, Appl |
| 14 | 24 | 3.0 | 24 | 14 | US-10-074-246-48 | Sequence 48, Appl |
| 15 | 24 | 3.0 | 685 | 14 | US-10-074-246-70 | Sequence 70, Appl |
| 16 | 24 | 3.0 | 686 | 14 | US-10-074-246-69 | Sequence 69, Appl |
| 17 | 22 | 2.7 | 22 | 9 | US-09-817-014-72 | Sequence 72, Appl |
| 18 | 22 | 2.7 | 22 | 14 | US-10-074-246-25 | Sequence 25, Appl |
| 19 | 22 | 2.7 | 22 | 16 | US-10-056-229-72 | Sequence 72, Appl |
| 20 | 22 | 2.7 | 219 | 14 | US-10-074-246-73 | Sequence 73, Appl |
| c 21 | 20 | 2.5 | 20 | 14 | US-10-074-246-1 | Sequence 1, Appli |
| 22 | 20 | 2.5 | 816 | 17 | US-10-369-493-35898 | Sequence 35898, A |
| 23 | 20 | 2.5 | 1491 | 18 | US-10-425-114-22932 | Sequence 22932, A |
| 24 | 20 | 2.5 | 1491 | 20 | US-10-425-115-76519 | Sequence 76519, A |
| 25 | 19 | 2.4 | 19 | 14 | US-10-074-246-52 | Sequence 52, Appl |
| 26 | 19 | 2.4 | 116 | 14 | US-10-074-246-74 | Sequence 74, Appl |
| c 27 | 19 | 2.4 | 334 | 20 | US-10-425-115-23733 | Sequence 23733, A |
| 28 | 19 | 2.4 | 705 | 20 | US-10-425-115-76518 | Sequence 76518, A |
| 29 | 19 | 2.4 | 717 | 9 | US-09-986-621-7 | Sequence 7, Appli |
| 30 | 19 | 2.4 | 717 | 10 | US-09-986-625-7 | Sequence 7, Appli |
| 31 | 19 | 2.4 | 717 | 16 | US-10-292-951-7 | Sequence 7, Appli |
| 32 | 19 | 2.4 | 717 | 17 | US-10-382-844-7 | Sequence 7, Appli |
| 33 | 19 | 2.4 | 765 | 9 | US-09-986-621-21 | Sequence 21, Appl |
| 34 | 19 | 2.4 | 765 | 10 | US-09-986-625-21 | Sequence 21, Appl |
| 35 | 19 | 2.4 | 765 | 16 | US-10-292-951-21 | Sequence 21, Appl |
| 36 | 19 | 2.4 | 765 | 17 | US-10-382-844-21 | Sequence 21, Appl |
| 37 | 19 | 2.4 | 886 | 20 | US-10-425-115-9429 | Sequence 9429, Ap |
| 38 | 19 | 2.4 | 1456 | 16 | US-10-292-951-37 | Sequence 37, Appl |
| 39 | 19 | 2.4 | 1456 | 17 | US-10-382-844-37 | Sequence 37, Appl |
| c 40 | 19 | 2.4 | 1456 | 19 | US-10-437-963-82805 | Sequence 82805, A |
| c 41 | 19 | 2.4 | 1478 | 20 | US-10-363-345A-16713 | Sequence 16713, A |
| 42 | 19 | 2.4 | 1478 | 20 | US-10-363-345A-16714 | Sequence 16714, A |
| c 43 | 19 | 2.4 | 1478 | 21 | US-10-363-483A-16713 | Sequence 16713, A |
| 44 | 19 | 2.4 | 1478 | 21 | US-10-363-483A-16714 | Sequence 16714, A |
| 45 | 19 | 2.4 | 1488 | 9 | US-09-986-621-8 | Sequence 8, Appli |

Search completed: July 12, 2005, 21:34:28
Job time : 644 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 18:22:18 ; Search time 3388 Seconds
(without alignments)
9010.491 Million cell updates/sec

Title: US-10-074-246-65
Perfect score: 802
Sequence: 1 tcatagcaggcctcctcttg.....tggctgcgtacttcgccagc 802

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 19

Total number of hits satisfying chosen parameters: 163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | % Query | | DB | ID | Description |
|--------|-----|-------|------------|--------|----|----------|--------------------|
| | | | Match | Length | | | |
| c | 1 | 20 | 2.5 | 339 | 5 | BP087522 | BP087522 BP087522 |
| c | 2 | 20 | 2.5 | 439 | 6 | CD036612 | CD036612 mgsu010xL |
| | 3 | 20 | 2.5 | 642 | 5 | BP125333 | BP125333 BP125333 |
| | 4 | 20 | 2.5 | 693 | 8 | BZ654250 | BZ654250 OGANC18TC |
| c | 5 | 20 | 2.5 | 709 | 9 | CG101385 | CG101385 PUIDS38TD |
| c | 6 | 20 | 2.5 | 788 | 9 | CG368128 | CG368128 OGYBX73TH |

| | | | | | | | | |
|---|----|----|-----|------|---|----------|----------|-----------|
| | 7 | 20 | 2.5 | 790 | 9 | CG101383 | CG101383 | PUIDS38TB |
| c | 8 | 20 | 2.5 | 794 | 4 | BM415165 | BM415165 | OP20237 M |
| | 9 | 20 | 2.5 | 807 | 8 | CC360524 | CC360524 | PUHHB49TD |
| c | 10 | 20 | 2.5 | 811 | 8 | BZ640143 | BZ640143 | OGAOY76TC |
| | 11 | 20 | 2.5 | 820 | 9 | CC717618 | CC717618 | OGOAK51TH |
| c | 12 | 20 | 2.5 | 836 | 2 | BE641565 | BE641565 | Cri2_3_K0 |
| c | 13 | 20 | 2.5 | 836 | 9 | CG355150 | CG355150 | OG0FI18TV |
| | 14 | 20 | 2.5 | 841 | 9 | CG128824 | CG128824 | PUFSB83TB |
| | 15 | 20 | 2.5 | 843 | 9 | CG350861 | CG350861 | OGXFO45TH |
| c | 16 | 20 | 2.5 | 858 | 9 | CG334280 | CG334280 | OG0FN56TH |
| | 17 | 20 | 2.5 | 859 | 9 | CG297677 | CG297677 | OG3DH69TH |
| c | 18 | 20 | 2.5 | 866 | 9 | CG310598 | CG310598 | OGWGW48TH |
| | 19 | 20 | 2.5 | 881 | 9 | CG310605 | CG310605 | OGWGW48TV |
| | 20 | 20 | 2.5 | 881 | 9 | CG368142 | CG368142 | OGYBX73TV |
| c | 21 | 20 | 2.5 | 884 | 9 | CC717628 | CC717628 | OGOAK51TV |
| | 22 | 20 | 2.5 | 923 | 9 | CG334290 | CG334290 | OG0FN56TV |
| | 23 | 20 | 2.5 | 925 | 9 | CG363674 | CG363674 | OG1CR45TV |
| c | 24 | 20 | 2.5 | 933 | 9 | CG456197 | CG456197 | PUIJX77TD |
| | 25 | 20 | 2.5 | 1025 | 9 | CG456153 | CG456153 | PUIJX77TB |
| c | 26 | 20 | 2.5 | 1487 | 2 | BF698864 | BF698864 | 602126433 |
| | 27 | 20 | 2.5 | 1513 | 9 | AG152149 | AG152149 | Pan trogl |
| c | 28 | 19 | 2.4 | 139 | 8 | CC380210 | CC380210 | PUHGX06TD |
| c | 29 | 19 | 2.4 | 148 | 9 | CL303432 | CL303432 | M051C08 G |
| c | 30 | 19 | 2.4 | 309 | 5 | BW575850 | BW575850 | BW575850 |
| | 31 | 19 | 2.4 | 332 | 1 | AV903172 | AV903172 | AV903172 |
| | 32 | 19 | 2.4 | 335 | 4 | BM848612 | BM848612 | K-EST0128 |
| c | 33 | 19 | 2.4 | 343 | 6 | CB655053 | CB655053 | OSJNEc08B |
| | 34 | 19 | 2.4 | 356 | 1 | AA280978 | AA280978 | zs97f03.r |
| c | 35 | 19 | 2.4 | 372 | 1 | AB009130 | AB009130 | AB009130 |
| | 36 | 19 | 2.4 | 404 | 5 | BY032959 | BY032959 | BY032959 |
| | 37 | 19 | 2.4 | 433 | 5 | BW509786 | BW509786 | BW509786 |
| | 38 | 19 | 2.4 | 511 | 2 | BE302649 | BE302649 | ba73f02.y |
| | 39 | 19 | 2.4 | 520 | 1 | AV864667 | AV864667 | AV864667 |
| | 40 | 19 | 2.4 | 523 | 9 | CG617736 | CG617736 | OST311668 |
| | 41 | 19 | 2.4 | 531 | 9 | CG653478 | CG653478 | OST418882 |
| | 42 | 19 | 2.4 | 544 | 9 | CG662435 | CG662435 | OST445990 |
| | 43 | 19 | 2.4 | 560 | 9 | CG645739 | CG645739 | OST390727 |
| | 44 | 19 | 2.4 | 580 | 5 | BP302387 | BP302387 | BP302387 |
| | 45 | 19 | 2.4 | 583 | 5 | BP235848 | BP235848 | BP235848 |

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 07:50:25 ; Search time 5482.32 Seconds
(without alignments)
7088.436 Million cell updates/sec

Title: US-10-074-246-65
Perfect score: 802
Sequence: 1 tcatagcaggcctcctcttg.....tggctgcgtacttcgccagc 802

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|---------------|-------|------------|--------|----|----------|--------------------|
| | | Match | Length | | | |
| 1 | 802 | 100.0 | 802 | 6 | AX513136 | AX513136 Sequence |
| 2 | 802 | 100.0 | 327650 | 1 | BX248337 | BX248337 Mycobacte |
| 3 | 802 | 100.0 | 349306 | 1 | BX842575 | BX842575 Mycobacte |

| | | | | | | |
|----|-------|-------|--------|---|-------------|--------------------|
| 4 | 801.6 | 100.0 | 110000 | 1 | AE000516_10 | Continuation (11 o |
| 5 | 626.4 | 78.1 | 628 | 6 | AX513137 | AX513137 Sequence |
| 6 | 449.2 | 56.0 | 611 | 6 | BD171688 | BD171688 Identific |
| 7 | 447.6 | 55.8 | 611 | 6 | BD171689 | BD171689 Identific |
| 8 | 416.6 | 51.9 | 712 | 6 | AX513135 | AX513135 Sequence |
| 9 | 408.6 | 50.9 | 785 | 6 | AX513132 | AX513132 Sequence |
| 10 | 407.6 | 50.8 | 881 | 6 | AX513129 | AX513129 Sequence |
| 11 | 407.6 | 50.8 | 1832 | 1 | MP34KDA | X68102 Mycobacteri |
| 12 | 407.6 | 50.8 | 1839 | 6 | A28087 | A28087 M.paratuber |
| 13 | 407.6 | 50.8 | 3200 | 1 | AF411607 | AF411607 Mycobacte |
| 14 | 407.6 | 50.8 | 303855 | 1 | AE017230 | AE017230 Mycobacte |
| 15 | 406 | 50.6 | 1839 | 6 | AR209771 | AR209771 Sequence |
| 16 | 384.6 | 48.0 | 685 | 6 | AX513141 | AX513141 Sequence |
| 17 | 383.8 | 47.9 | 691 | 6 | AX513133 | AX513133 Sequence |
| 18 | 375.2 | 46.8 | 686 | 6 | AX513140 | AX513140 Sequence |
| 19 | 370.8 | 46.2 | 707 | 6 | AX513139 | AX513139 Sequence |
| 20 | 369 | 46.0 | 369 | 6 | BD171700 | BD171700 Identific |
| 21 | 354.8 | 44.2 | 698 | 6 | AX513134 | AX513134 Sequence |
| 22 | 351.4 | 43.8 | 745 | 6 | AX513131 | AX513131 Sequence |
| 23 | 321.4 | 40.1 | 323 | 6 | BD171699 | BD171699 Identific |
| 24 | 320.2 | 39.9 | 642 | 6 | AX513130 | AX513130 Sequence |
| 25 | 269.2 | 33.6 | 110000 | 1 | AP006618_27 | Continuation (28 o |
| 26 | 266.6 | 33.2 | 37304 | 1 | MLCL373 | AL035500 Mycobacte |
| 27 | 266.6 | 33.2 | 344050 | 1 | MLEPRTN1 | AL583917 Mycobacte |
| 28 | 239 | 29.8 | 668 | 6 | BD171691 | BD171691 Identific |
| 29 | 238 | 29.7 | 729 | 6 | AX513142 | AX513142 Sequence |
| 30 | 229.6 | 28.6 | 669 | 6 | BD171690 | BD171690 Identific |
| 31 | 229.4 | 28.6 | 724 | 6 | BD171686 | BD171686 Identific |
| 32 | 220 | 27.4 | 690 | 6 | BD171684 | BD171684 Identific |
| 33 | 220 | 27.4 | 690 | 6 | BD171685 | BD171685 Identific |
| 34 | 216.4 | 27.0 | 1058 | 6 | AR169193 | AR169193 Sequence |
| 35 | 216.4 | 27.0 | 1058 | 6 | BD205858 | BD205858 Compounds |
| 36 | 216.4 | 27.0 | 1058 | 6 | CQ785444 | CQ785444 Sequence |
| 37 | 216.4 | 27.0 | 1058 | 6 | AR182483 | AR182483 Sequence |
| 38 | 216.4 | 27.0 | 1058 | 6 | AR194866 | AR194866 Sequence |
| 39 | 216.4 | 27.0 | 1058 | 6 | AR233138 | AR233138 Sequence |
| 40 | 216.4 | 27.0 | 1058 | 6 | AR353343 | AR353343 Sequence |
| 41 | 216.4 | 27.0 | 1058 | 6 | AX429637 | AX429637 Sequence |
| 42 | 216.4 | 27.0 | 1058 | 6 | AX832622 | AX832622 Sequence |
| 43 | 216.4 | 27.0 | 1058 | 6 | BD006366 | BD006366 Compounds |
| 44 | 216.4 | 27.0 | 1058 | 6 | BD006486 | BD006486 Compounds |
| 45 | 216.4 | 27.0 | 1058 | 6 | BD069326 | BD069326 Compounds |

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 07:50:25 ; Search time 960.512 Seconds
(without alignments)
4942.816 Million cell updates/sec

Title: US-10-074-246-65
Perfect score: 802
Sequence: 1 tcatagcaggcctcctcttg.....tggctgcgtacttcgccagc 802

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|------------|-------|---------|--------|----|-------------|--------------------|
| | | Match | Length | | | |
| 1 | 802 | 100.0 | 802 | 6 | ABS70084 | Abs70084 Mycobacte |
| 2 | 802 | 100.0 | 802 | 8 | ABX10110 | Abx10110 M. tuberc |
| 3 | 802 | 100.0 | 110000 | 4 | AAI99682_10 | Continuation (11 o |
| 4 | 801.6 | 100.0 | 110000 | 4 | AAI99683_10 | Continuation (11 o |
| 5 | 648 | 80.8 | 648 | 8 | ABX10126 | Abx10126 M. tuberc |

| | | | | | | | |
|----|-------|------|------|---|----------|----------|-----------|
| 6 | 643.2 | 80.2 | 648 | 8 | ABX10127 | Abx10127 | M. bovis |
| 7 | 626.4 | 78.1 | 628 | 6 | ABS70085 | Abs70085 | Mycobacte |
| 8 | 626.4 | 78.1 | 628 | 8 | ABX10111 | Abx10111 | M. bovis |
| 9 | 416.6 | 51.9 | 712 | 6 | ABS70083 | Abs70083 | Mycobacte |
| 10 | 416.6 | 51.9 | 712 | 8 | ABX10109 | Abx10109 | M. szulga |
| 11 | 410.8 | 51.2 | 881 | 8 | ABX10113 | Abx10113 | M. avium |
| 12 | 408.6 | 50.9 | 785 | 6 | ABS70080 | Abs70080 | Mycobacte |
| 13 | 408.6 | 50.9 | 785 | 8 | ABX10104 | Abx10104 | M. gordon |
| 14 | 407.6 | 50.8 | 881 | 6 | ABS70077 | Abs70077 | Mycobacte |
| 15 | 407.6 | 50.8 | 1839 | 2 | AAQ29147 | Aaq29147 | DNA encod |
| 16 | 384.6 | 48.0 | 685 | 6 | ABS70089 | Abs70089 | Mycobacte |
| 17 | 384.6 | 48.0 | 685 | 8 | ABX10116 | Abx10116 | M. ulcera |
| 18 | 384.6 | 48.0 | 705 | 8 | ABX10129 | Abx10129 | M. ulcera |
| 19 | 383.8 | 47.9 | 691 | 6 | ABS70081 | Abs70081 | Mycobacte |
| 20 | 383.8 | 47.9 | 741 | 8 | ABX10105 | Abx10105 | M. intrac |
| 21 | 383.8 | 47.9 | 761 | 8 | ABX10124 | Abx10124 | M. malmoe |
| 22 | 380 | 47.4 | 706 | 8 | ABX10128 | Abx10128 | M. marinu |
| 23 | 375.2 | 46.8 | 686 | 6 | ABS70088 | Abs70088 | Mycobacte |
| 24 | 375.2 | 46.8 | 686 | 8 | ABX10115 | Abx10115 | M. marinu |
| 25 | 370.8 | 46.2 | 707 | 6 | ABS70087 | Abs70087 | Mycobacte |
| 26 | 370.8 | 46.2 | 727 | 8 | ABX10123 | Abx10123 | M. paratu |
| 27 | 370.8 | 46.2 | 727 | 8 | ABX10122 | Abx10122 | M. avium |
| 28 | 369.2 | 46.0 | 707 | 8 | ABX10114 | Abx10114 | M. paratu |
| 29 | 359 | 44.8 | 570 | 8 | ABX10133 | Abx10133 | M. szulga |
| 30 | 358 | 44.6 | 768 | 8 | ABX10125 | Abx10125 | M. simae |
| 31 | 354.8 | 44.2 | 698 | 6 | ABS70082 | Abs70082 | Mycobacte |
| 32 | 354.8 | 44.2 | 748 | 8 | ABX10108 | Abx10108 | M. simae |
| 33 | 351.4 | 43.8 | 745 | 6 | ABS70079 | Abs70079 | Mycobacte |
| 34 | 351.4 | 43.8 | 745 | 8 | ABX10107 | Abx10107 | M. malmoe |
| 35 | 326.8 | 40.7 | 631 | 8 | ABX10131 | Abx10131 | M. kansas |
| 36 | 325 | 40.5 | 662 | 8 | ABX10130 | Abx10130 | M. gastri |
| 37 | 320.2 | 39.9 | 642 | 6 | ABS70078 | Abs70078 | Mycobacte |
| 38 | 320.2 | 39.9 | 642 | 8 | ABX10106 | Abx10106 | M. kansas |
| 39 | 292 | 36.4 | 588 | 8 | ABX10132 | Abx10132 | M. gordon |
| 40 | 238 | 29.7 | 729 | 6 | ABS70090 | Abs70090 | Mycobacte |
| 41 | 238 | 29.7 | 729 | 8 | ABX10117 | Abx10117 | M. leprae |
| 42 | 236.2 | 29.5 | 727 | 8 | ABX10134 | Abx10134 | M. leprae |
| 43 | 216.4 | 27.0 | 1058 | 2 | AAT91444 | Aat91444 | Mycobacte |
| 44 | 216.4 | 27.0 | 1058 | 2 | AAT91508 | Aat91508 | Mycobacte |
| 45 | 216.4 | 27.0 | 1058 | 2 | AAV44383 | Aav44383 | Mycobacte |

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 10:18:20 ; Search time 283.234 Seconds
(without alignments)
4633.247 Million cell updates/sec

Title: US-10-074-246-65
Perfect score: 802
Sequence: 1 tcatagcaggcctcctcttg.....tggctgcgtacttcgccagc 802

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | % Match | Query Length | DB ID | Description |
|--------|-----|-------|------------|-----------------|----------|-------------------|
| | 1 | 802 | 100.0 | 4411529 | 3 | US-09-103-840A-1 |
| | 2 | 801.6 | 100.0 | 4403765 | 3 | US-09-103-840A-2 |
| | 3 | 406 | 50.6 | 1839 | 3 | US-08-122-458D-10 |
| | 4 | 216.4 | 27.0 | 1058 | 3 | US-08-818-112-45 |
| | 5 | 216.4 | 27.0 | 1058 | 3 | US-08-818-111-45 |
| | 6 | 216.4 | 27.0 | 1058 | 3 | US-09-056-556-45 |
| | 7 | 216.4 | 27.0 | 1058 | 3 | US-09-072-596-45 |
| | 8 | 216.4 | 27.0 | 1058 | 4 | US-09-072-967-45 |
| | 9 | 89.2 | 11.1 | 597 | 3 | US-08-122-458D-17 |
| c | 10 | 71.6 | 8.9 | 1185 | 4 | US-09-894-844-71 |
| c | 11 | 71.6 | 8.9 | 4403765 | 3 | US-09-103-840A-2 |
| c | 12 | 71.6 | 8.9 | 4411529 | 3 | US-09-103-840A-1 |

| | | | | | | | |
|---|----|------|-----|-------|---|----------------------|-------------------|
| c | 13 | 70.4 | 8.8 | 888 | 3 | US-09-655-270A-6 | Sequence 6, Appli |
| c | 14 | 70.4 | 8.8 | 888 | 3 | US-09-651-941-6 | Sequence 6, Appli |
| c | 15 | 70.4 | 8.8 | 888 | 3 | US-09-955-597-6 | Sequence 6, Appli |
| c | 16 | 70.4 | 8.8 | 12508 | 3 | US-09-655-270A-1 | Sequence 1, Appli |
| c | 17 | 70.4 | 8.8 | 12523 | 3 | US-09-651-941-1 | Sequence 1, Appli |
| c | 18 | 70.4 | 8.8 | 12523 | 3 | US-09-955-597-1 | Sequence 1, Appli |
| c | 19 | 61 | 7.6 | 825 | 4 | US-09-266-965-58 | Sequence 58, Appl |
| | 20 | 61 | 7.6 | 53500 | 4 | US-09-266-965-76 | Sequence 76, Appl |
| | 21 | 50.2 | 6.3 | 402 | 4 | US-09-252-991A-15772 | Sequence 15772, A |
| c | 22 | 50.2 | 6.3 | 999 | 4 | US-09-252-991A-15890 | Sequence 15890, A |
| c | 23 | 50.2 | 6.3 | 1086 | 4 | US-09-252-991A-15921 | Sequence 15921, A |
| | 24 | 50.2 | 6.3 | 1284 | 4 | US-09-252-991A-15802 | Sequence 15802, A |
| c | 25 | 50.2 | 6.3 | 3390 | 4 | US-09-902-540-6647 | Sequence 6647, Ap |
| | 26 | 50.2 | 6.3 | 3393 | 4 | US-09-902-540-514 | Sequence 514, App |
| c | 27 | 48.8 | 6.1 | 1185 | 4 | US-09-252-991A-3103 | Sequence 3103, Ap |
| c | 28 | 48.8 | 6.1 | 2592 | 4 | US-09-252-991A-3003 | Sequence 3003, Ap |
| c | 29 | 46 | 5.7 | 1149 | 4 | US-09-266-965-41 | Sequence 41, Appl |
| c | 30 | 45 | 5.6 | 4284 | 4 | US-09-902-540-3289 | Sequence 3289, Ap |
| | 31 | 45 | 5.6 | 17727 | 4 | US-09-902-540-1152 | Sequence 1152, Ap |
| | 32 | 44.4 | 5.5 | 450 | 4 | US-09-252-991A-664 | Sequence 664, App |
| | 33 | 44.4 | 5.5 | 1728 | 4 | US-09-252-991A-616 | Sequence 616, App |
| c | 34 | 42.6 | 5.3 | 1155 | 4 | US-09-902-540-4958 | Sequence 4958, Ap |
| c | 35 | 42.6 | 5.3 | 1170 | 4 | US-09-252-991A-5515 | Sequence 5515, Ap |
| | 36 | 42.6 | 5.3 | 1434 | 4 | US-09-252-991A-5626 | Sequence 5626, Ap |
| c | 37 | 42.6 | 5.3 | 1992 | 4 | US-09-252-991A-5567 | Sequence 5567, Ap |
| c | 38 | 42.6 | 5.3 | 6975 | 4 | US-09-902-540-2386 | Sequence 2386, Ap |
| | 39 | 42.6 | 5.3 | 17315 | 4 | US-09-902-540-1103 | Sequence 1103, Ap |
| c | 40 | 42.6 | 5.3 | 27219 | 4 | US-09-902-540-1244 | Sequence 1244, Ap |
| c | 41 | 42.4 | 5.3 | 30001 | 1 | US-08-125-468-1 | Sequence 1, Appli |
| c | 42 | 42.4 | 5.3 | 30001 | 2 | US-08-474-933-1 | Sequence 1, Appli |
| c | 43 | 42.2 | 5.3 | 47981 | 4 | US-09-679-279-1 | Sequence 1, Appli |
| c | 44 | 42 | 5.2 | 1695 | 4 | US-09-902-540-8849 | Sequence 8849, Ap |
| c | 45 | 42 | 5.2 | 9993 | 4 | US-09-902-540-942 | Sequence 942, App |

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 11:13:07 ; Search time 1166.73 Seconds
(without alignments)
4315.680 Million cell updates/sec

Title: US-10-074-246-65
Perfect score: 802
Sequence: 1 tcatagcaggcctcctcttg.....tggctgcgtacttcgccagc 802

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6330945 seqs, 3139162390, residues

Total number of hits satisfying chosen parameters: 12661890

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | % | | | | | |
|--------|-------|-------|---------|--------|----------------------|----|-------------------|
| No. | Score | Query | Match | Length | DB | ID | Description |
| 1 | 802 | 100.0 | 802 | 14 | US-10-074-246-65 | | Sequence 65, Appl |
| 2 | 626.4 | 78.1 | 628 | 14 | US-10-074-246-66 | | Sequence 66, Appl |
| 3 | 416.6 | 51.9 | 712 | 14 | US-10-074-246-64 | | Sequence 64, Appl |
| 4 | 408.6 | 50.9 | 785 | 14 | US-10-074-246-61 | | Sequence 61, Appl |
| 5 | 407.6 | 50.8 | 881 | 14 | US-10-074-246-58 | | Sequence 58, Appl |
| 6 | 384.6 | 48.0 | 685 | 14 | US-10-074-246-70 | | Sequence 70, Appl |
| 7 | 383.8 | 47.9 | 691 | 14 | US-10-074-246-62 | | Sequence 62, Appl |
| 8 | 375.2 | 46.8 | 686 | 14 | US-10-074-246-69 | | Sequence 69, Appl |
| 9 | 370.8 | 46.2 | 707 | 14 | US-10-074-246-68 | | Sequence 68, Appl |
| 10 | 354.8 | 44.2 | 698 | 14 | US-10-074-246-63 | | Sequence 63, Appl |
| 11 | 351.4 | 43.8 | 745 | 14 | US-10-074-246-60 | | Sequence 60, Appl |
| 12 | 320.2 | 39.9 | 642 | 14 | US-10-074-246-59 | | Sequence 59, Appl |
| 13 | 238 | 29.7 | 729 | 14 | US-10-074-246-71 | | Sequence 71, Appl |
| 14 | 216.4 | 27.0 | 1058 | 15 | US-10-193-002-45 | | Sequence 45, Appl |
| 15 | 216.4 | 27.0 | 1058 | 15 | US-10-084-843-45 | | Sequence 45, Appl |
| 16 | 216.4 | 27.0 | 1058 | 24 | US-11-028-898-45 | | Sequence 45, Appl |
| 17 | 122.6 | 15.3 | 9025608 | 15 | US-10-156-761-1 | | Sequence 1, Appli |
| c 18 | 121.8 | 15.2 | 825 | 15 | US-10-156-761-7462 | | Sequence 7462, Ap |
| 19 | 117.2 | 14.6 | 400 | 14 | US-10-074-246-67 | | Sequence 67, Appl |
| c 20 | 71.6 | 8.9 | 1185 | 9 | US-09-894-844-71 | | Sequence 71, Appl |
| c 21 | 71.6 | 8.9 | 1185 | 17 | US-10-388-902-71 | | Sequence 71, Appl |
| c 22 | 71.6 | 8.9 | 1185 | 18 | US-10-647-089-71 | | Sequence 71, Appl |
| c 23 | 71.6 | 8.9 | 1188 | 17 | US-10-282-122A-28727 | | Sequence 28727, A |
| c 24 | 70.4 | 8.8 | 888 | 9 | US-09-955-597-6 | | Sequence 6, Appli |
| c 25 | 70.4 | 8.8 | 12523 | 9 | US-09-955-597-1 | | Sequence 1, Appli |
| c 26 | 63.2 | 7.9 | 9521 | 18 | US-10-168-663-18 | | Sequence 18, Appl |
| 27 | 63.2 | 7.9 | 9521 | 18 | US-10-168-663-19 | | Sequence 19, Appl |
| c 28 | 61.8 | 7.7 | 816 | 15 | US-10-156-761-581 | | Sequence 581, App |
| c 29 | 61.8 | 7.7 | 927 | 15 | US-10-156-761-3786 | | Sequence 3786, Ap |
| c 30 | 61.8 | 7.7 | 9025608 | 15 | US-10-156-761-1 | | Sequence 1, Appli |
| c 31 | 61 | 7.6 | 825 | 10 | US-09-953-348-58 | | Sequence 58, Appl |
| c 32 | 61 | 7.6 | 825 | 15 | US-10-267-255-58 | | Sequence 58, Appl |
| 33 | 61 | 7.6 | 53500 | 10 | US-09-953-348-76 | | Sequence 76, Appl |
| 34 | 61 | 7.6 | 53500 | 15 | US-10-267-255-76 | | Sequence 76, Appl |
| c 35 | 57 | 7.1 | 927 | 15 | US-10-156-761-6872 | | Sequence 6872, Ap |
| c 36 | 54.2 | 6.8 | 978 | 15 | US-10-156-761-2643 | | Sequence 2643, Ap |
| c 37 | 50.2 | 6.3 | 1002 | 9 | US-09-815-242-7774 | | Sequence 7774, Ap |
| c 38 | 47.8 | 6.0 | 1014 | 15 | US-10-156-761-6996 | | Sequence 6996, Ap |
| c 39 | 47.8 | 6.0 | 1287 | 15 | US-10-156-761-832 | | Sequence 832, App |
| c 40 | 46 | 5.7 | 1149 | 10 | US-09-953-348-41 | | Sequence 41, Appl |
| c 41 | 46 | 5.7 | 1149 | 15 | US-10-267-255-41 | | Sequence 41, Appl |
| 42 | 45.8 | 5.7 | 1371 | 17 | US-10-282-122A-15021 | | Sequence 15021, A |
| 43 | 45.6 | 5.7 | 1818 | 17 | US-10-282-122A-14315 | | Sequence 14315, A |
| c 44 | 45.4 | 5.7 | 1704 | 17 | US-10-282-122A-13510 | | Sequence 13510, A |
| 45 | 45.4 | 5.7 | 1752 | 17 | US-10-282-122A-13696 | | Sequence 13696, A |

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 10:06:45 ; Search time 6338.48 Seconds
(without alignments)
4816.222 Million cell updates/sec

Title: US-10-074-246-65
Perfect score: 802
Sequence: 1 tcatagcaggcctcctcttg.....tggctgcgtacttcgccagc 802

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | % Query Match | Length | DB | ID | Description |
|--------|-----|-------|---------------------|--------|----|----------|--------------------|
| c | 1 | 58.2 | 7.3 | 925 | 9 | CNS0091P | AL053013 Drosophil |
| | 2 | 56.4 | 7.0 | 925 | 9 | CNS0091P | AL053013 Drosophil |
| c | 3 | 56.4 | 7.0 | 935 | 9 | CNS006XK | AL066051 Drosophil |
| c | 4 | 51.4 | 6.4 | 985 | 6 | CA981964 | CA981964 AGENCOURT |
| c | 5 | 50.6 | 6.3 | 645 | 9 | CNS012I3 | AL101589 Drosophil |
| c | 6 | 50.2 | 6.3 | 1028 | 8 | BZ550423 | BZ550423 pacsl-60_ |
| c | 7 | 50.2 | 6.3 | 1399 | 8 | BZ554759 | BZ554759 pacsl-60_ |
| c | 8 | 48.8 | 6.1 | 1101 | 9 | CNS017SY | AL108460 Drosophil |
| | 9 | 47.8 | 6.0 | 645 | 9 | CNS012I3 | AL101589 Drosophil |

| | | | | | | | | |
|---|----|------|-----|------|---|----------|----------|-----------|
| | 10 | 47.2 | 5.9 | 1752 | 9 | CL972165 | CL972165 | OsIFCC041 |
| | 11 | 47 | 5.9 | 1339 | 4 | BM458211 | BM458211 | AGENCOURT |
| c | 12 | 46.8 | 5.8 | 932 | 9 | CNS0072Q | AL066742 | Drosophil |
| | 13 | 46.6 | 5.8 | 1038 | 7 | CK206930 | CK206930 | FGAS01854 |
| | 14 | 46.2 | 5.8 | 832 | 9 | AG108460 | AG108460 | Pan trogl |
| c | 15 | 46 | 5.7 | 1462 | 9 | AG441877 | AG441877 | Mus muscu |
| | 16 | 45.8 | 5.7 | 802 | 8 | BZ675208 | BZ675208 | PUBAL48TD |
| | 17 | 45.8 | 5.7 | 1452 | 9 | AG032979 | AG032979 | Pan trogl |
| c | 18 | 45.4 | 5.7 | 650 | 8 | CC331276 | CC331276 | OGUAF63TH |
| c | 19 | 45.4 | 5.7 | 711 | 7 | CO520370 | CO520370 | 3530_1_13 |
| | 20 | 45.4 | 5.7 | 725 | 6 | CD423375 | CD423375 | SA1_28_D1 |
| | 21 | 45.4 | 5.7 | 1328 | 9 | AG043615 | AG043615 | Pan trogl |
| c | 22 | 45.2 | 5.6 | 767 | 8 | AQ847229 | AQ847229 | LMAJFV1_1 |
| c | 23 | 45.2 | 5.6 | 851 | 6 | CB908312 | CB908312 | tric084xp |
| | 24 | 44.6 | 5.6 | 932 | 9 | CNS0072Q | AL066742 | Drosophil |
| c | 25 | 44.6 | 5.6 | 961 | 5 | BQ673489 | BQ673489 | AGENCOURT |
| | 26 | 44.4 | 5.5 | 1021 | 8 | BZ559395 | BZ559395 | pacs2-164 |
| c | 27 | 44.4 | 5.5 | 1045 | 8 | BZ564504 | BZ564504 | pacs2-164 |
| c | 28 | 44.4 | 5.5 | 1119 | 8 | BZ560644 | BZ560644 | pacs2-164 |
| | 29 | 44.4 | 5.5 | 1516 | 4 | BG809984 | BG809984 | mgct002xd |
| | 30 | 44.2 | 5.5 | 776 | 9 | CG218187 | CG218187 | OGYAP34TV |
| | 31 | 44.2 | 5.5 | 935 | 9 | CNS006XK | AL066051 | Drosophil |
| c | 32 | 44 | 5.5 | 513 | 8 | BZ896393 | BZ896393 | NaRP9_014 |
| | 33 | 44 | 5.5 | 1598 | 9 | AG030579 | AG030579 | Pan trogl |
| | 34 | 43.8 | 5.5 | 553 | 2 | BF277572 | BF277572 | GA_Eb003 |
| c | 35 | 43.8 | 5.5 | 794 | 8 | BZ564793 | BZ564793 | pacs2-164 |
| | 36 | 43.6 | 5.4 | 317 | 4 | BI417136 | BI417136 | 949053F04 |
| | 37 | 43.6 | 5.4 | 317 | 4 | BI674168 | BI674168 | 949053F04 |
| | 38 | 43.6 | 5.4 | 549 | 4 | BI358830 | BI358830 | 949041E06 |
| | 39 | 43.6 | 5.4 | 606 | 4 | BI595873 | BI595873 | 949073A06 |
| | 40 | 43.4 | 5.4 | 430 | 6 | CB644339 | CB644339 | OSJNEb05I |
| c | 41 | 43.4 | 5.4 | 618 | 7 | CF303450 | CF303450 | ABF1--02- |
| | 42 | 43.4 | 5.4 | 676 | 6 | CB649863 | CB649863 | OSJNEb14A |
| | 43 | 43.4 | 5.4 | 692 | 6 | CB654140 | CB654140 | OSJNEc05N |
| | 44 | 43.4 | 5.4 | 697 | 6 | CB656121 | CB656121 | OSJNEc10B |

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 07:50:25 ; Search time 4832.92 Seconds
 (without alignments)
 7088.436 Million cell updates/sec

Title: US-10-074-246-68
 Perfect score: 707
 Sequence: 1 tcgtagctggcttctctgctc.....aaaaggcagtgggaagcaaca 707

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : GenEmbl:*
 1: gb_ba:*
 2: gb_htg:*
 3: gb_in:*
 4: gb_om:*
 5: gb_ov:*
 6: gb_pat:*
 7: gb_ph:*
 8: gb_pl:*
 9: gb_pr:*
 10: gb_ro:*
 11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|------------|-------|---------|--------|----|----------|--------------------|
| | | Match | Length | | | |
| 1 | 707 | 100.0 | 707 | 6 | AX513139 | AX513139 Sequence |
| 2 | 707 | 100.0 | 1832 | 1 | MP34KDA | X68102 Mycobacteri |
| 3 | 707 | 100.0 | 1839 | 6 | A28087 | A28087 M.paratuber |

| | | | | | | | |
|----|-------|-------|--------|---|-------------|--------------------|-----------|
| 4 | 707 | 100.0 | 3200 | 1 | AF411607 | AF411607 | Mycobacte |
| 5 | 707 | 100.0 | 303855 | 1 | AE017230 | AE017230 | Mycobacte |
| 6 | 705.4 | 99.8 | 881 | 6 | AX513129 | AX513129 | Sequence |
| 7 | 705.4 | 99.8 | 1839 | 6 | AR209771 | AR209771 | Sequence |
| 8 | 529 | 74.8 | 690 | 6 | BD171685 | BD171685 | Identific |
| 9 | 527.4 | 74.6 | 690 | 6 | BD171684 | BD171684 | Identific |
| 10 | 426.6 | 60.3 | 691 | 6 | AX513133 | AX513133 | Sequence |
| 11 | 422 | 59.7 | 448 | 6 | BD171701 | BD171701 | Identific |
| 12 | 411.8 | 58.2 | 698 | 6 | AX513134 | AX513134 | Sequence |
| 13 | 383.8 | 54.3 | 685 | 6 | AX513141 | AX513141 | Sequence |
| 14 | 376 | 53.2 | 686 | 6 | AX513140 | AX513140 | Sequence |
| 15 | 370.8 | 52.4 | 802 | 6 | AX513136 | AX513136 | Sequence |
| 16 | 370.8 | 52.4 | 110000 | 1 | AE000516_10 | Continuation (11 o | |
| 17 | 370.8 | 52.4 | 327650 | 1 | BX248337 | BX248337 | Mycobacte |
| 18 | 370.8 | 52.4 | 349306 | 1 | BX842575 | BX842575 | Mycobacte |
| 19 | 369.2 | 52.2 | 628 | 6 | AX513137 | AX513137 | Sequence |
| 20 | 350.6 | 49.6 | 785 | 6 | AX513132 | AX513132 | Sequence |
| 21 | 344.2 | 48.7 | 712 | 6 | AX513135 | AX513135 | Sequence |
| 22 | 330.2 | 46.7 | 642 | 6 | AX513130 | AX513130 | Sequence |
| 23 | 312.6 | 44.2 | 745 | 6 | AX513131 | AX513131 | Sequence |
| 24 | 283.8 | 40.1 | 110000 | 1 | AP006618_27 | Continuation (28 o | |
| 25 | 265 | 37.5 | 724 | 6 | BD171686 | BD171686 | Identific |
| 26 | 257.8 | 36.5 | 731 | 6 | BD171687 | BD171687 | Identific |
| 27 | 241.8 | 34.2 | 37304 | 1 | MLCL373 | AL035500 | Mycobacte |
| 28 | 241.8 | 34.2 | 344050 | 1 | MLEPRTN1 | AL583917 | Mycobacte |
| 29 | 236.4 | 33.4 | 729 | 6 | AX513142 | AX513142 | Sequence |
| 30 | 229.8 | 32.5 | 668 | 6 | BD171691 | BD171691 | Identific |
| 31 | 222 | 31.4 | 669 | 6 | BD171690 | BD171690 | Identific |
| 32 | 215.4 | 30.5 | 217 | 6 | BD171702 | BD171702 | Identific |
| 33 | 211.6 | 29.9 | 611 | 6 | BD171688 | BD171688 | Identific |
| 34 | 210 | 29.7 | 611 | 6 | BD171689 | BD171689 | Identific |
| 35 | 187.2 | 26.5 | 594 | 6 | BD171693 | BD171693 | Identific |
| 36 | 182.4 | 25.8 | 533 | 6 | BD171695 | BD171695 | Identific |
| 37 | 173.6 | 24.6 | 625 | 6 | BD171692 | BD171692 | Identific |
| 38 | 168.2 | 23.8 | 551 | 6 | BD171694 | BD171694 | Identific |
| 39 | 164.2 | 23.2 | 369 | 6 | BD171700 | BD171700 | Identific |
| 40 | 147.4 | 20.8 | 343 | 6 | BD171697 | BD171697 | Identific |
| 41 | 144.8 | 20.5 | 323 | 6 | BD171699 | BD171699 | Identific |
| 42 | 144.8 | 20.5 | 37586 | 6 | AX191745 | AX191745 | Sequence |
| 43 | 144.8 | 20.5 | 110000 | 1 | AE000516_24 | Continuation (25 o | |
| 44 | 144.8 | 20.5 | 306050 | 1 | BX248341 | BX248341 | Mycobacte |
| 45 | 144.8 | 20.5 | 346186 | 1 | BX842578 | BX842578 | Mycobacte |

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 07:50:25 ; Search time 846.735 Seconds
(without alignments)
4942.816 Million cell updates/sec

Title: US-10-074-246-68
Perfect score: 707
Sequence: 1 tcgtagctggcttctctgctc.....aaaaggcagtgggaagcaaca 707

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | % | | | | |
|--------|-------|-------|-------|--------|----------|--------------------|
| No. | Score | Query | Match | Length | ID | Description |
| | | | DB | | | |
| 1 | 707 | 100.0 | 707 | 6 | ABS70087 | Abs70087 Mycobacte |
| 2 | 707 | 100.0 | 727 | 8 | ABX10123 | Abx10123 M. paratu |
| 3 | 707 | 100.0 | 1839 | 2 | AAQ29147 | Aaq29147 DNA encod |
| 4 | 705.4 | 99.8 | 707 | 8 | ABX10114 | Abx10114 M. paratu |
| 5 | 705.4 | 99.8 | 727 | 8 | ABX10122 | Abx10122 M. avium |

| | | | | | | |
|----|-------|------|--------|---|-------------|--------------------|
| 6 | 705.4 | 99.8 | 881 | 6 | ABS70077 | Abs70077 Mycobacte |
| 7 | 702.2 | 99.3 | 881 | 8 | ABX10113 | Abx10113 M. avium |
| 8 | 433.4 | 61.3 | 761 | 8 | ABX10124 | Abx10124 M. malmoe |
| 9 | 430.2 | 60.8 | 741 | 8 | ABX10105 | Abx10105 M. intrac |
| 10 | 426.6 | 60.3 | 691 | 6 | ABS70081 | Abs70081 Mycobacte |
| 11 | 415 | 58.7 | 768 | 8 | ABX10125 | Abx10125 M. simae |
| 12 | 411.8 | 58.2 | 698 | 6 | ABS70082 | Abs70082 Mycobacte |
| 13 | 411.8 | 58.2 | 748 | 8 | ABX10108 | Abx10108 M. simae |
| 14 | 391.8 | 55.4 | 705 | 8 | ABX10129 | Abx10129 M. ulcera |
| 15 | 383.8 | 54.3 | 685 | 6 | ABS70089 | Abs70089 Mycobacte |
| 16 | 383.8 | 54.3 | 685 | 8 | ABX10116 | Abx10116 M. ulcera |
| 17 | 380.8 | 53.9 | 706 | 8 | ABX10128 | Abx10128 M. marinu |
| 18 | 376 | 53.2 | 686 | 6 | ABS70088 | Abs70088 Mycobacte |
| 19 | 376 | 53.2 | 686 | 8 | ABX10115 | Abx10115 M. marinu |
| 20 | 370.8 | 52.4 | 648 | 8 | ABX10126 | Abx10126 M. tuberc |
| 21 | 370.8 | 52.4 | 648 | 8 | ABX10127 | Abx10127 M. bovis |
| 22 | 370.8 | 52.4 | 802 | 6 | ABS70084 | Abs70084 Mycobacte |
| 23 | 370.8 | 52.4 | 802 | 8 | ABX10110 | Abx10110 M. tuberc |
| 24 | 370.8 | 52.4 | 110000 | 4 | AAI99682_10 | Continuation (11 o |
| 25 | 370.8 | 52.4 | 110000 | 4 | AAI99683_10 | Continuation (11 o |
| 26 | 369.2 | 52.2 | 628 | 6 | ABS70085 | Abs70085 Mycobacte |
| 27 | 369.2 | 52.2 | 628 | 8 | ABX10111 | Abx10111 M. bovis |
| 28 | 352.2 | 49.8 | 570 | 8 | ABX10133 | Abx10133 M. szulga |
| 29 | 350.6 | 49.6 | 631 | 8 | ABX10131 | Abx10131 M. kansas |
| 30 | 350.6 | 49.6 | 785 | 6 | ABS70080 | Abs70080 Mycobacte |
| 31 | 350.6 | 49.6 | 785 | 8 | ABX10104 | Abx10104 M. gordon |
| 32 | 344.2 | 48.7 | 712 | 6 | ABS70083 | Abs70083 Mycobacte |
| 33 | 344.2 | 48.7 | 712 | 8 | ABX10109 | Abx10109 M. szulga |
| 34 | 330.2 | 46.7 | 642 | 6 | ABS70078 | Abs70078 Mycobacte |
| 35 | 330.2 | 46.7 | 642 | 8 | ABX10106 | Abx10106 M. kansas |
| 36 | 330.2 | 46.7 | 662 | 8 | ABX10130 | Abx10130 M. gastri |
| 37 | 312.6 | 44.2 | 745 | 6 | ABS70079 | Abs70079 Mycobacte |
| 38 | 312.6 | 44.2 | 745 | 8 | ABX10107 | Abx10107 M. malmoe |
| 39 | 309.4 | 43.8 | 588 | 8 | ABX10132 | Abx10132 M. gordon |
| 40 | 254.8 | 36.0 | 727 | 8 | ABX10134 | Abx10134 M. leprae |
| 41 | 236.4 | 33.4 | 729 | 6 | ABS70090 | Abs70090 Mycobacte |
| 42 | 236.4 | 33.4 | 729 | 8 | ABX10117 | Abx10117 M. leprae |
| 43 | 150 | 21.2 | 373 | 8 | ABX10135 | Abx10135 M. intrac |
| 44 | 144.8 | 20.5 | 110000 | 4 | AAI99682_24 | Continuation (25 o |
| 45 | 144.8 | 20.5 | 110000 | 4 | AAI99683_24 | Continuation (25 o |

Search completed: July 12, 2005, 14:48:36
Job time : 848.735 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 10:18:20 ; Search time 249.684 Seconds
(without alignments)
4633.247 Million cell updates/sec

Title: US-10-074-246-68
Perfect score: 707
Sequence: 1 tcgtagctggcttcctcgtc.....aaaaggcagtggaagcaaca 707

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | % Query Match | Length | DB | ID | Description |
|--------|-----|-------|---------------------|---------|----|-------------------|-------------------|
| | 1 | 705.4 | 99.8 | 1839 | 3 | US-08-122-458D-10 | Sequence 10, Appl |
| | 2 | 370.8 | 52.4 | 4403765 | 3 | US-09-103-840A-2 | Sequence 2, Appli |
| | 3 | 370.8 | 52.4 | 4411529 | 3 | US-09-103-840A-1 | Sequence 1, Appli |
| c | 4 | 70.4 | 10.0 | 888 | 3 | US-09-655-270A-6 | Sequence 6, Appli |
| c | 5 | 70.4 | 10.0 | 888 | 3 | US-09-651-941-6 | Sequence 6, Appli |
| c | 6 | 70.4 | 10.0 | 888 | 3 | US-09-955-597-6 | Sequence 6, Appli |
| c | 7 | 70.4 | 10.0 | 12508 | 3 | US-09-655-270A-1 | Sequence 1, Appli |
| c | 8 | 70.4 | 10.0 | 12523 | 3 | US-09-651-941-1 | Sequence 1, Appli |
| c | 9 | 70.4 | 10.0 | 12523 | 3 | US-09-955-597-1 | Sequence 1, Appli |

| | | | | | | | |
|---|----|------|-----|---------|---|----------------------|-------------------|
| c | 10 | 65.4 | 9.3 | 1185 | 4 | US-09-894-844-71 | Sequence 71, Appl |
| c | 11 | 65.4 | 9.3 | 4403765 | 3 | US-09-103-840A-2 | Sequence 2, Appli |
| c | 12 | 65.4 | 9.3 | 4411529 | 3 | US-09-103-840A-1 | Sequence 1, Appli |
| c | 13 | 64.4 | 9.1 | 825 | 4 | US-09-266-965-58 | Sequence 58, Appl |
| | 14 | 64.4 | 9.1 | 53500 | 4 | US-09-266-965-76 | Sequence 76, Appl |
| c | 15 | 62 | 8.8 | 795 | 4 | US-09-266-965-57 | Sequence 57, Appl |
| c | 16 | 62 | 8.8 | 53500 | 4 | US-09-266-965-76 | Sequence 76, Appl |
| c | 17 | 56.4 | 8.0 | 4089 | 4 | US-09-902-540-7372 | Sequence 7372, Ap |
| | 18 | 56.4 | 8.0 | 4090 | 4 | US-09-902-540-706 | Sequence 706, App |
| c | 19 | 54.8 | 7.8 | 1185 | 4 | US-09-252-991A-3103 | Sequence 3103, Ap |
| c | 20 | 54.8 | 7.8 | 2592 | 4 | US-09-252-991A-3003 | Sequence 3003, Ap |
| c | 21 | 52.8 | 7.5 | 328 | 3 | US-09-060-756-406 | Sequence 406, App |
| c | 22 | 52.8 | 7.5 | 328 | 4 | US-09-670-314-406 | Sequence 406, App |
| c | 23 | 52.2 | 7.4 | 355 | 3 | US-09-060-756-390 | Sequence 390, App |
| c | 24 | 52.2 | 7.4 | 355 | 4 | US-09-670-314-390 | Sequence 390, App |
| c | 25 | 52.2 | 7.4 | 438 | 3 | US-09-060-756-112 | Sequence 112, App |
| c | 26 | 52.2 | 7.4 | 438 | 4 | US-09-670-314-112 | Sequence 112, App |
| c | 27 | 51.8 | 7.3 | 308 | 3 | US-09-060-756-532 | Sequence 532, App |
| c | 28 | 51.8 | 7.3 | 308 | 4 | US-09-670-314-532 | Sequence 532, App |
| | 29 | 51.4 | 7.3 | 402 | 4 | US-09-252-991A-15772 | Sequence 15772, A |
| c | 30 | 51.4 | 7.3 | 999 | 4 | US-09-252-991A-15890 | Sequence 15890, A |
| c | 31 | 51.4 | 7.3 | 1086 | 4 | US-09-252-991A-15921 | Sequence 15921, A |
| | 32 | 51.4 | 7.3 | 1284 | 4 | US-09-252-991A-15802 | Sequence 15802, A |
| c | 33 | 51.2 | 7.2 | 6975 | 4 | US-09-902-540-2386 | Sequence 2386, Ap |
| | 34 | 51.2 | 7.2 | 17315 | 4 | US-09-902-540-1103 | Sequence 1103, Ap |
| c | 35 | 50.4 | 7.1 | 3390 | 4 | US-09-902-540-6647 | Sequence 6647, Ap |
| | 36 | 50.4 | 7.1 | 3393 | 4 | US-09-902-540-514 | Sequence 514, App |
| c | 37 | 49.2 | 7.0 | 30001 | 1 | US-08-125-468-1 | Sequence 1, Appli |
| c | 38 | 49.2 | 7.0 | 30001 | 2 | US-08-474-933-1 | Sequence 1, Appli |
| c | 39 | 48.2 | 6.8 | 303 | 3 | US-09-060-756-468 | Sequence 468, App |
| c | 40 | 48.2 | 6.8 | 303 | 4 | US-09-670-314-468 | Sequence 468, App |
| c | 41 | 48.2 | 6.8 | 2427 | 4 | US-09-902-540-5377 | Sequence 5377, Ap |
| c | 42 | 48.2 | 6.8 | 34552 | 4 | US-09-902-540-1262 | Sequence 1262, Ap |
| | 43 | 47.6 | 6.7 | 1221 | 4 | US-09-252-991A-13701 | Sequence 13701, A |
| c | 44 | 47.6 | 6.7 | 1365 | 4 | US-09-252-991A-13442 | Sequence 13442, A |
| c | 45 | 47.6 | 6.7 | 2337 | 4 | US-09-252-991A-2034 | Sequence 2034, Ap |

Search completed: July 12, 2005, 18:32:49
Job time : 272.684 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 11:13:07 ; Search time 1028.52 Seconds
(without alignments)
4315.680 Million cell updates/sec

Title: US-10-074-246-68
Perfect score: 707
Sequence: 1 tcgtagctggcttcctcgtc.....aaaaggcagtgggaagcaaca 707

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6330945 seqs, 3139162390 residues

Total number of hits satisfying chosen parameters: 12661890

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | % | | | | |
|--------|-------|-------------|---------|----|----------------------|-------------------|
| No. | Score | Query Match | Length | DB | ID | Description |
| 1 | 707 | 100.0 | 707 | 14 | US-10-074-246-68 | Sequence 68, Appl |
| 2 | 705.4 | 99.8 | 881 | 14 | US-10-074-246-58 | Sequence 58, Appl |
| 3 | 426.6 | 60.3 | 691 | 14 | US-10-074-246-62 | Sequence 62, Appl |
| 4 | 411.8 | 58.2 | 698 | 14 | US-10-074-246-63 | Sequence 63, Appl |
| 5 | 383.8 | 54.3 | 685 | 14 | US-10-074-246-70 | Sequence 70, Appl |
| 6 | 376 | 53.2 | 686 | 14 | US-10-074-246-69 | Sequence 69, Appl |
| 7 | 370.8 | 52.4 | 802 | 14 | US-10-074-246-65 | Sequence 65, Appl |
| 8 | 369.2 | 52.2 | 628 | 14 | US-10-074-246-66 | Sequence 66, Appl |
| 9 | 350.6 | 49.6 | 785 | 14 | US-10-074-246-61 | Sequence 61, Appl |
| 10 | 344.2 | 48.7 | 712 | 14 | US-10-074-246-64 | Sequence 64, Appl |
| 11 | 330.2 | 46.7 | 642 | 14 | US-10-074-246-59 | Sequence 59, Appl |
| 12 | 312.6 | 44.2 | 745 | 14 | US-10-074-246-60 | Sequence 60, Appl |
| 13 | 236.4 | 33.4 | 729 | 14 | US-10-074-246-71 | Sequence 71, Appl |
| 14 | 139.4 | 19.7 | 216 | 14 | US-10-074-246-57 | Sequence 57, Appl |
| 15 | 138.2 | 19.5 | 9025608 | 15 | US-10-156-761-1 | Sequence 1, Appli |
| c 16 | 137.8 | 19.5 | 825 | 15 | US-10-156-761-7462 | Sequence 7462, Ap |
| c 17 | 89.6 | 12.7 | 816 | 15 | US-10-156-761-581 | Sequence 581, App |
| c 18 | 89.6 | 12.7 | 9025608 | 15 | US-10-156-761-1 | Sequence 1, Appli |
| c 19 | 79 | 11.2 | 978 | 15 | US-10-156-761-2643 | Sequence 2643, Ap |
| c 20 | 78.4 | 11.1 | 9521 | 18 | US-10-168-663-18 | Sequence 18, Appl |
| 21 | 78.4 | 11.1 | 9521 | 18 | US-10-168-663-19 | Sequence 19, Appl |
| c 22 | 70.4 | 10.0 | 888 | 9 | US-09-955-597-6 | Sequence 6, Appli |
| c 23 | 70.4 | 10.0 | 12523 | 9 | US-09-955-597-1 | Sequence 1, Appli |
| c 24 | 67 | 9.5 | 1068 | 15 | US-10-156-761-4239 | Sequence 4239, Ap |
| c 25 | 66.8 | 9.4 | 927 | 15 | US-10-156-761-3786 | Sequence 3786, Ap |
| c 26 | 65.4 | 9.3 | 1185 | 9 | US-09-894-844-71 | Sequence 71, Appl |
| c 27 | 65.4 | 9.3 | 1185 | 17 | US-10-388-902-71 | Sequence 71, Appl |
| c 28 | 65.4 | 9.3 | 1185 | 18 | US-10-647-089-71 | Sequence 71, Appl |
| c 29 | 65.4 | 9.3 | 1188 | 17 | US-10-282-122A-28727 | Sequence 28727, A |
| c 30 | 64.4 | 9.1 | 825 | 10 | US-09-953-348-58 | Sequence 58, Appl |
| c 31 | 64.4 | 9.1 | 825 | 15 | US-10-267-255-58 | Sequence 58, Appl |
| 32 | 64.4 | 9.1 | 53500 | 10 | US-09-953-348-76 | Sequence 76, Appl |
| 33 | 64.4 | 9.1 | 53500 | 15 | US-10-267-255-76 | Sequence 76, Appl |
| c 34 | 62.8 | 8.9 | 927 | 15 | US-10-156-761-6872 | Sequence 6872, Ap |
| c 35 | 62.6 | 8.9 | 1287 | 15 | US-10-156-761-832 | Sequence 832, App |
| c 36 | 62 | 8.8 | 795 | 10 | US-09-953-348-57 | Sequence 57, Appl |
| c 37 | 62 | 8.8 | 795 | 15 | US-10-267-255-57 | Sequence 57, Appl |
| c 38 | 62 | 8.8 | 53500 | 10 | US-09-953-348-76 | Sequence 76, Appl |
| c 39 | 62 | 8.8 | 53500 | 15 | US-10-267-255-76 | Sequence 76, Appl |
| c 40 | 61.6 | 8.7 | 1101 | 15 | US-10-156-761-2265 | Sequence 2265, Ap |
| c 41 | 58 | 8.2 | 1719 | 15 | US-10-156-761-3854 | Sequence 3854, Ap |
| c 42 | 57.8 | 8.2 | 552 | 19 | US-10-437-963-79213 | Sequence 79213, A |
| c 43 | 57.8 | 8.2 | 1119 | 15 | US-10-156-761-1197 | Sequence 1197, Ap |
| c 44 | 56.4 | 8.0 | 3018 | 19 | US-10-437-963-77223 | Sequence 77223, A |
| c 45 | 56.4 | 8.0 | 11058 | 15 | US-10-156-761-3629 | Sequence 3629, Ap |

Search completed: July 12, 2005, 20:49:00
Job time : 2703.52 secs

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 10:06:45 ; Search time 5587.67 Seconds
(without alignments)
4816.222 Million cell updates/sec

Title: US-10-074-246-68
Perfect score: 707
Sequence: 1 tcgtagctggcttcctcgtc.....aaaaggcagtggaagcaaca 707

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | % Query | | DB | ID | Description |
|--------|-----|-------|------------|--------|----|----------|--------------------|
| | | | Match | Length | | | |
| c | 1 | 64.2 | 9.1 | 935 | 9 | CNS006XK | AL066051 Drosophil |
| | 2 | 63 | 8.9 | 925 | 9 | CNS0091P | AL053013 Drosophil |
| c | 3 | 62.2 | 8.8 | 925 | 9 | CNS0091P | AL053013 Drosophil |
| | 4 | 60.2 | 8.5 | 605 | 9 | CC648836 | CC648836 OGUJL60TV |
| c | 5 | 60.2 | 8.5 | 873 | 9 | CC682998 | CC682998 OGWEA16TH |
| | 6 | 58.8 | 8.3 | 935 | 9 | CNS006XK | AL066051 Drosophil |

| | | | | | | | | |
|---|----|------|-----|------|---|----------|----------|-----------|
| | 7 | 57 | 8.1 | 1542 | 9 | AG032943 | AG032943 | Pan trogl |
| c | 8 | 56.6 | 8.0 | 754 | 9 | CC610065 | CC610065 | OGUJX42TV |
| c | 9 | 56.4 | 8.0 | 1045 | 8 | BZ564504 | BZ564504 | pacs2-164 |
| c | 10 | 56.4 | 8.0 | 2856 | 9 | CL966856 | CL966856 | OsIFCC014 |
| | 11 | 56 | 7.9 | 932 | 9 | CNS0072Q | AL066742 | Drosophil |
| | 12 | 55.8 | 7.9 | 849 | 9 | CC718810 | CC718810 | OGLBV70TV |
| | 13 | 55.8 | 7.9 | 859 | 8 | CC328293 | CC328293 | OGOBE04TV |
| | 14 | 55.8 | 7.9 | 929 | 9 | CG290273 | CG290273 | OGZAU73TV |
| c | 15 | 55.8 | 7.9 | 968 | 9 | CG274354 | CG274354 | OG2BE18TV |
| c | 16 | 55.4 | 7.8 | 822 | 9 | CG290264 | CG290264 | OGZAU73TH |
| | 17 | 55 | 7.8 | 502 | 8 | BZ411257 | BZ411257 | OGAAC57TF |
| c | 18 | 55 | 7.8 | 1307 | 9 | CL486103 | CL486103 | SAIL_427_ |
| c | 19 | 54.6 | 7.7 | 552 | 9 | CL980743 | CL980743 | OsIFCC045 |
| c | 20 | 54.6 | 7.7 | 552 | 9 | CL980748 | CL980748 | OsIFCC045 |
| | 21 | 54.2 | 7.7 | 1152 | 9 | AG076818 | AG076818 | Pan trogl |
| c | 22 | 54 | 7.6 | 903 | 9 | AG072453 | AG072453 | Pan trogl |
| c | 23 | 53.4 | 7.6 | 1041 | 5 | BQ652051 | BQ652051 | AGENCOURT |
| c | 24 | 53.2 | 7.5 | 1009 | 9 | CNS010EW | AL098882 | Drosophil |
| c | 25 | 52.4 | 7.4 | 1046 | 5 | BQ643604 | BQ643604 | AGENCOURT |
| | 26 | 52.4 | 7.4 | 1569 | 9 | AG341503 | AG341503 | Mus muscu |
| | 27 | 52.2 | 7.4 | 1319 | 9 | CL498921 | CL498921 | SAIL_661_ |
| c | 28 | 51.6 | 7.3 | 762 | 9 | CG308028 | CG308028 | OGVEH70TH |
| c | 29 | 51.6 | 7.3 | 982 | 5 | BQ687717 | BQ687717 | AGENCOURT |
| c | 30 | 51.4 | 7.3 | 1399 | 8 | BZ554759 | BZ554759 | pacs1-60_ |
| c | 31 | 51.2 | 7.2 | 931 | 7 | CK412737 | CK412737 | AUF_IpGi1 |
| | 32 | 50.8 | 7.2 | 414 | 8 | BH630331 | BH630331 | 1007088A0 |
| c | 33 | 50.8 | 7.2 | 638 | 9 | CC657126 | CC657126 | OGDAG42TC |
| c | 34 | 50.8 | 7.2 | 646 | 8 | BZ974761 | BZ974761 | PUGJE03TB |
| | 35 | 50.8 | 7.2 | 663 | 7 | CF624053 | CF624053 | zmrws05_0 |
| | 36 | 50.8 | 7.2 | 718 | 8 | BZ974765 | BZ974765 | PUGJE03TD |
| c | 37 | 50.6 | 7.2 | 932 | 9 | CNS0072Q | AL066742 | Drosophil |
| c | 38 | 50.4 | 7.1 | 1375 | 2 | AW727483 | AW727483 | GA_Ea001 |
| c | 39 | 50.4 | 7.1 | 1473 | 9 | CL975386 | CL975386 | OsIFCC027 |
| c | 40 | 50.2 | 7.1 | 776 | 9 | CNS010RY | AL099352 | Drosophil |
| c | 41 | 50.2 | 7.1 | 839 | 9 | CNS004NB | AL054280 | Drosophil |
| c | 42 | 50 | 7.1 | 557 | 5 | BU037493 | BU037493 | 946139F05 |
| c | 43 | 50 | 7.1 | 589 | 5 | BQ778943 | BQ778943 | 946115F10 |
| c | 44 | 50 | 7.1 | 688 | 6 | CA830993 | CA830993 | 1117014B0 |
| | 45 | 49.8 | 7.0 | 411 | 8 | AQ961051 | AQ961051 | LERFI83TR |

Sequence: 1 gccgtccagtcgttaatgtcgc 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | % Match | Query Length | DB | ID | Description |
|--------|-----|-------|------------|-----------------|----|-------------|--------------------|
| | 1 | 22 | 100.0 | 22 | 6 | BD171663 | BD171663 Identific |
| | 2 | 22 | 100.0 | 22 | 6 | AX278539 | AX278539 Sequence |
| | 3 | 22 | 100.0 | 22 | 6 | AX513096 | AX513096 Sequence |
| | 4 | 22 | 100.0 | 24 | 6 | AX513119 | AX513119 Sequence |
| | 5 | 22 | 100.0 | 323 | 6 | BD171699 | BD171699 Identific |
| | 6 | 22 | 100.0 | 369 | 6 | BD171700 | BD171700 Identific |
| | 7 | 22 | 100.0 | 611 | 6 | BD171688 | BD171688 Identific |
| | 8 | 22 | 100.0 | 611 | 6 | BD171689 | BD171689 Identific |
| | 9 | 22 | 100.0 | 628 | 6 | AX513137 | AX513137 Sequence |
| | 10 | 22 | 100.0 | 802 | 6 | AX513136 | AX513136 Sequence |
| | 11 | 22 | 100.0 | 110000 | 1 | AE000516_10 | Continuation (11 o |
| | 12 | 22 | 100.0 | 327650 | 1 | BX248337 | BX248337 Mycobacte |
| | 13 | 22 | 100.0 | 349306 | 1 | BX842575 | BX842575 Mycobacte |
| | 14 | 19 | 86.4 | 19 | 6 | AX513123 | AX513123 Sequence |
| c | 15 | 18.8 | 85.5 | 3276 | 6 | A44223 | A44223 Sequence 4 |
| c | 16 | 18.8 | 85.5 | 3276 | 6 | A72710 | A72710 Sequence 4 |

| | | | | | | | |
|---|----|------|------|--------|----|-----------|--------------------|
| c | 17 | 18.8 | 85.5 | 3276 | 6 | AR408850 | AR408850 Sequence |
| c | 18 | 18.8 | 85.5 | 3276 | 6 | AX002862 | AX002862 Sequence |
| c | 19 | 18.8 | 85.5 | 4314 | 8 | GLE18738 | Y18738 Gracilariop |
| c | 20 | 17.8 | 80.9 | 214922 | 2 | AC150991 | AC150991 Bos tauru |
| c | 21 | 17.8 | 80.9 | 226889 | 14 | AC146905 | AC146905 Human Her |
| c | 22 | 17.8 | 80.9 | 229209 | 14 | AC146907 | AC146907 Human Her |
| | 23 | 17.8 | 80.9 | 229354 | 6 | AR474465 | AR474465 Sequence |
| | 24 | 17.8 | 80.9 | 229354 | 6 | AR475529 | AR475529 Sequence |
| | 25 | 17.8 | 80.9 | 229354 | 6 | AX686187 | AX686187 Sequence |
| | 26 | 17.8 | 80.9 | 229354 | 14 | HEHCMVCG | X17403 Human cytom |
| | 27 | 17.8 | 80.9 | 229483 | 14 | AC146851 | AC146851 Human Her |
| c | 28 | 17.8 | 80.9 | 229700 | 14 | AC146904 | AC146904 Human Her |
| | 29 | 17.8 | 80.9 | 231236 | 14 | AY315197 | AY315197 Human her |
| c | 30 | 17.8 | 80.9 | 233739 | 14 | AC146999 | AC146999 Human Her |
| | 31 | 17.8 | 80.9 | 234881 | 14 | AC146906 | AC146906 Human Her |
| | 32 | 17.8 | 80.9 | 235645 | 14 | AY446894 | AY446894 Human her |
| c | 33 | 17.2 | 78.2 | 97095 | 2 | AC141824 | AC141824 Apis mell |
| c | 34 | 17.2 | 78.2 | 160042 | 2 | AL365211 | AL365211 Homo sapi |
| | 35 | 17.2 | 78.2 | 175968 | 9 | AC018684 | AC018684 Homo sapi |
| c | 36 | 17.2 | 78.2 | 300425 | 1 | AP005022 | AP005022 Streptomy |
| | 37 | 17.2 | 78.2 | 302070 | 1 | AP005223 | AP005223 Corynebac |
| | 38 | 16.8 | 76.4 | 70290 | 2 | AC100833 | AC100833 Homo sapi |
| | 39 | 16.8 | 76.4 | 105689 | 2 | AC136152 | AC136152 Rattus no |
| | 40 | 16.8 | 76.4 | 110000 | 1 | U00096_02 | Continuation (3 of |
| c | 41 | 16.8 | 76.4 | 113253 | 2 | AC092356 | AC092356 Homo sapi |
| | 42 | 16.8 | 76.4 | 128824 | 1 | ECU73857 | U73857 Escherichia |
| | 43 | 16.8 | 76.4 | 155862 | 9 | AC018464 | AC018464 Homo sapi |
| c | 44 | 16.8 | 76.4 | 156349 | 10 | AC117550 | AC117550 Mus muscu |
| | 45 | 16.8 | 76.4 | 162167 | 2 | AC019271 | AC019271 Homo sapi |

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 07:50:25 ; Search time 26.3482 Seconds
(without alignments)
4942.816 Million cell updates/sec

Title: US-10-074-246-25
Perfect score: 22
Sequence: 1 gccgtccagtcgttaatgtcgc 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

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- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|------------|-------|---------|--------|----|----------|--------------------|
| | | Match | Length | | | |
| 1 | 22 | 100.0 | 22 | 6 | ABS70044 | Abs70044 Mycobacte |
| 2 | 22 | 100.0 | 22 | 6 | ABA81861 | Aba81861 M tubercu |
| 3 | 22 | 100.0 | 22 | 8 | ABX10101 | Abx10101 M. tuberc |
| 4 | 22 | 100.0 | 24 | 6 | ABS70067 | Abs70067 Mycobacte |
| 5 | 22 | 100.0 | 628 | 6 | ABS70085 | Abs70085 Mycobacte |

| | | | | | | | |
|---|----|------|-------|--------|----|-------------|--------------------|
| | 6 | 22 | 100.0 | 628 | 8 | ABX10111 | Abx10111 M. bovis |
| | 7 | 22 | 100.0 | 648 | 8 | ABX10126 | Abx10126 M. tuberc |
| | 8 | 22 | 100.0 | 648 | 8 | ABX10127 | Abx10127 M. bovis |
| | 9 | 22 | 100.0 | 802 | 6 | ABS70084 | Abs70084 Mycobacte |
| | 10 | 22 | 100.0 | 802 | 8 | ABX10110 | Abx10110 M. tuberc |
| | 11 | 22 | 100.0 | 110000 | 4 | AAI99682_10 | Continuation (11 o |
| | 12 | 22 | 100.0 | 110000 | 4 | AAI99683_10 | Continuation (11 o |
| | 13 | 19 | 86.4 | 19 | 6 | ABS70071 | Abs70071 Mycobacte |
| c | 14 | 18.8 | 85.5 | 3276 | 2 | AAQ88050 | Aaq88050 Glucan Ly |
| c | 15 | 18.8 | 85.5 | 3276 | 2 | AAQ87604 | Aaq87604 Fungus-in |
| c | 16 | 18.8 | 85.5 | 3276 | 2 | AAV84193 | Aav84193 Gracilari |
| | 17 | 17.8 | 80.9 | 229354 | 6 | ABQ74179 | Abq74179 Human cyt |
| | 18 | 17.4 | 79.1 | 43011 | 12 | ADN01941 | Adn01941 Staphyloc |
| c | 19 | 17.2 | 78.2 | 907 | 8 | ABZ52394 | Abz52394 Aspergill |
| c | 20 | 16.8 | 76.4 | 2383 | 5 | AAS89875 | Aas89875 DNA encod |
| c | 21 | 16.8 | 76.4 | 2451 | 5 | AAS85748 | Aas85748 DNA encod |
| c | 22 | 15.8 | 71.8 | 417 | 8 | ABZ52746 | Abz52746 Aspergill |
| c | 23 | 15.8 | 71.8 | 617 | 3 | AAF08207 | Aaf08207 Fusarium |
| c | 24 | 15.8 | 71.8 | 1044 | 10 | ABZ66697 | Abz66697 Orthosomy |
| | 25 | 15.8 | 71.8 | 1140 | 6 | ABQ22020 | Abq22020 Oligonucl |
| c | 26 | 15.8 | 71.8 | 1140 | 6 | ABQ22021 | Abq22021 Oligonucl |
| | 27 | 15.8 | 71.8 | 1362 | 4 | AAF60956 | Aaf60956 P. putida |
| c | 28 | 15.8 | 71.8 | 1377 | 8 | ACA53865 | Aca53865 Prokaryot |
| c | 29 | 15.8 | 71.8 | 1410 | 10 | ADG33797 | Adg33797 Actinomyc |
| c | 30 | 15.8 | 71.8 | 2000 | 8 | ADA71563 | Ada71563 Rice gene |
| | 31 | 15.8 | 71.8 | 3738 | 8 | ACA36064 | Aca36064 Prokaryot |
| | 32 | 15.8 | 71.8 | 3849 | 11 | ACH96678 | Ach96678 Klebsiell |
| c | 33 | 15.8 | 71.8 | 4316 | 10 | ADB69197 | Adb69197 C. neofor |
| | 34 | 15.8 | 71.8 | 37116 | 10 | ABZ66810 | Abz66810 Orthosomy |
| c | 35 | 15.8 | 71.8 | 109519 | 5 | AAS08693 | Aas08693 Micromono |
| c | 36 | 15.8 | 71.8 | 110000 | 10 | ADF77343_08 | Continuation (9 of |
| | 37 | 15.6 | 70.9 | 348 | 11 | ABD15073 | Abd15073 Pseudomon |
| | 38 | 15.6 | 70.9 | 690 | 6 | ABQ24858 | Abq24858 Oligonucl |
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| c | 40 | 15.6 | 70.9 | 852 | 4 | AAK91722 | Aak91722 Human cDN |
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| c | 42 | 15.6 | 70.9 | 852 | 12 | ADL28149 | Adl28149 5' end of |
| c | 43 | 15.6 | 70.9 | 852 | 12 | ADL30415 | Adl30415 5' end of |
| | 44 | 15.6 | 70.9 | 925 | 13 | ADS56904 | Ads56904 Bacterial |
| | 45 | 15.6 | 70.9 | 1086 | 12 | ADO48504 | Ado48504 Human 108 |

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 10:18:20 ; Search time 7.76952 Seconds
(without alignments)
4633.247 Million cell updates/sec

Title: US-10-074-246-25
Perfect score: 22
Sequence: 1 gccgtccagtcgttaatgtcgc 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| | 1 | 22 | 100.0 | 4403765 | 3 | US-09-103-840A-2 | Sequence 2, Appli |
| | 2 | 22 | 100.0 | 4411529 | 3 | US-09-103-840A-1 | Sequence 1, Appli |
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| c | 4 | 18.8 | 85.5 | 3276 | 4 | US-09-280-197-4 | Sequence 4, Appli |
| | 5 | 17.8 | 80.9 | 229354 | 4 | US-09-705-400-64 | Sequence 64, Appl |
| c | 6 | 16.8 | 76.4 | 1305 | 4 | US-09-902-540-4277 | Sequence 4277, Ap |
| | 7 | 16.8 | 76.4 | 26012 | 4 | US-09-902-540-1212 | Sequence 1212, Ap |
| c | 8 | 16.2 | 73.6 | 1145 | 3 | US-09-221-017B-944 | Sequence 944, App |
| c | 9 | 16.2 | 73.6 | 4800 | 4 | US-09-902-540-562 | Sequence 562, App |
| c | 10 | 16 | 72.7 | 765 | 4 | US-09-248-796A-1849 | Sequence 1849, Ap |
| | 11 | 15.8 | 71.8 | 3849 | 4 | US-09-489-039A-2473 | Sequence 2473, Ap |
| | 12 | 15.6 | 70.9 | 348 | 4 | US-09-252-991A-13677 | Sequence 13677, A |

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| | 13 | 15.6 | 70.9 | 486 | 4 | US-09-902-540-3038 | Sequence 3038, Ap |
| | 14 | 15.6 | 70.9 | 1557 | 3 | US-07-852-132A-12 | Sequence 12, Appl |
| | 15 | 15.6 | 70.9 | 1557 | 5 | PCT-US91-01327-12 | Sequence 12, Appl |
| | 16 | 15.6 | 70.9 | 1557 | 6 | 5248670-2 | Patent No. 5248670 |
| | 17 | 15.6 | 70.9 | 1557 | 6 | 5248670-2 | Patent No. 5248670 |
| | 18 | 15.6 | 70.9 | 1623 | 4 | US-09-489-039A-88 | Sequence 88, Appl |
| | 19 | 15.6 | 70.9 | 1992 | 4 | US-09-252-991A-13771 | Sequence 13771, A |
| c | 20 | 15.6 | 70.9 | 2175 | 4 | US-09-252-991A-13657 | Sequence 13657, A |
| c | 21 | 15.6 | 70.9 | 2292 | 4 | US-09-252-991A-13575 | Sequence 13575, A |
| c | 22 | 15.6 | 70.9 | 3279 | 4 | US-09-275-608-1 | Sequence 1, Appli |
| | 23 | 15.6 | 70.9 | 5105 | 4 | US-09-902-540-791 | Sequence 791, App |
| c | 24 | 15.6 | 70.9 | 27219 | 4 | US-09-902-540-1244 | Sequence 1244, Ap |
| | 25 | 15.6 | 70.9 | 87563 | 3 | US-09-453-702B-57 | Sequence 57, Appl |
| c | 26 | 15.6 | 70.9 | 154746 | 4 | US-09-827-688-8 | Sequence 8, Appli |
| | 27 | 15.2 | 69.1 | 601 | 4 | US-09-949-016-206008 | Sequence 206008, |
| | 28 | 15.2 | 69.1 | 601 | 4 | US-09-949-016-206009 | Sequence 206009, |
| c | 29 | 15.2 | 69.1 | 792 | 4 | US-09-976-594-511 | Sequence 511, App |
| | 30 | 15.2 | 69.1 | 851 | 3 | US-09-008-892-10 | Sequence 10, Appl |
| c | 31 | 15.2 | 69.1 | 897 | 4 | US-09-902-540-7777 | Sequence 7777, Ap |
| | 32 | 15.2 | 69.1 | 6250 | 4 | US-09-902-540-773 | Sequence 773, App |
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| c | 36 | 15 | 68.2 | 1572 | 4 | US-09-489-039A-5714 | Sequence 5714, Ap |
| c | 37 | 14.8 | 67.3 | 927 | 1 | US-08-499-568-1 | Sequence 1, Appli |
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| c | 39 | 14.8 | 67.3 | 930 | 4 | US-09-134-000C-3208 | Sequence 3208, Ap |
| c | 40 | 14.8 | 67.3 | 1180 | 4 | US-09-247-890-2 | Sequence 2, Appli |
| c | 41 | 14.8 | 67.3 | 1180 | 4 | US-09-724-969-2 | Sequence 2, Appli |
| c | 42 | 14.8 | 67.3 | 1180 | 4 | US-09-724-852-2 | Sequence 2, Appli |
| c | 43 | 14.8 | 67.3 | 1185 | 4 | US-09-247-890-1 | Sequence 1, Appli |
| c | 44 | 14.8 | 67.3 | 1185 | 4 | US-09-724-969-1 | Sequence 1, Appli |
| c | 45 | 14.8 | 67.3 | 1185 | 4 | US-09-724-852-1 | Sequence 1, Appli |

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 11:13:07 ; Search time 32.005 Seconds
(without alignments)
4315.680 Million cell updates/sec

Title: US-10-074-246-25
Perfect score: 22
Sequence: 1 gccgtccagtcgttaatgtcgc 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6330945 seqs, 3139162390 residues

Total number of hits satisfying chosen parameters: 12661890

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 22 | 100.0 | 22 | 14 | US-10-074-246-25 | Sequence 25, Appl |
| 3 | 22 | 100.0 | 22 | 16 | US-10-056-229-72 | Sequence 72, Appl |
| 4 | 22 | 100.0 | 24 | 14 | US-10-074-246-48 | Sequence 48, Appl |
| 5 | 22 | 100.0 | 628 | 14 | US-10-074-246-66 | Sequence 66, Appl |
| 6 | 22 | 100.0 | 802 | 14 | US-10-074-246-65 | Sequence 65, Appl |
| 7 | 19 | 86.4 | 19 | 14 | US-10-074-246-52 | Sequence 52, Appl |
| c 8 | 18.8 | 85.5 | 3276 | 9 | US-09-280-197-4 | Sequence 4, Appli |
| c 9 | 18.8 | 85.5 | 3276 | 9 | US-09-423-126-8 | Sequence 8, Appli |
| c 10 | 18.8 | 85.5 | 3276 | 17 | US-10-448-139-4 | Sequence 4, Appli |
| c 11 | 18.8 | 85.5 | 3276 | 21 | US-10-879-638-8 | Sequence 8, Appli |
| 12 | 17.8 | 80.9 | 218802 | 21 | US-10-897-508-1 | Sequence 1, Appli |
| c 13 | 17.2 | 78.2 | 9025608 | 15 | US-10-156-761-1 | Sequence 1, Appli |
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| c 15 | 16.2 | 73.6 | 408 | 20 | US-10-425-115-112345 | Sequence 112345, |
| c 16 | 16.2 | 73.6 | 1145 | 13 | US-10-194-163-944 | Sequence 944, App |
| c 17 | 16.2 | 73.6 | 1380 | 15 | US-10-156-761-5958 | Sequence 5958, Ap |
| c 18 | 16.2 | 73.6 | 2078 | 20 | US-10-425-115-51743 | Sequence 51743, A |
| c 19 | 16.2 | 73.6 | 2085 | 20 | US-10-739-930-2710 | Sequence 2710, Ap |
| 20 | 15.8 | 71.8 | 25 | 21 | US-10-719-900-182550 | Sequence 182550, |
| c 21 | 15.8 | 71.8 | 416 | 20 | US-10-425-115-5185 | Sequence 5185, Ap |
| c 22 | 15.8 | 71.8 | 617 | 20 | US-10-653-047-730 | Sequence 730, App |
| c 23 | 15.8 | 71.8 | 1041 | 11 | US-09-758-759-12 | Sequence 12, Appl |
| c 24 | 15.8 | 71.8 | 1044 | 17 | US-10-107-431-56 | Sequence 56, Appl |
| 25 | 15.8 | 71.8 | 1140 | 20 | US-10-363-345A-8611 | Sequence 8611, Ap |
| c 26 | 15.8 | 71.8 | 1140 | 20 | US-10-363-345A-8612 | Sequence 8612, Ap |
| 27 | 15.8 | 71.8 | 1140 | 21 | US-10-363-483A-8611 | Sequence 8611, Ap |
| c 28 | 15.8 | 71.8 | 1140 | 21 | US-10-363-483A-8612 | Sequence 8612, Ap |
| c 29 | 15.8 | 71.8 | 1377 | 17 | US-10-282-122A-41735 | Sequence 41735, A |
| c 30 | 15.8 | 71.8 | 1410 | 18 | US-10-417-700A-56 | Sequence 56, Appl |
| 31 | 15.8 | 71.8 | 3738 | 17 | US-10-282-122A-23934 | Sequence 23934, A |
| c 32 | 15.8 | 71.8 | 4316 | 17 | US-10-320-797-324 | Sequence 324, App |
| 33 | 15.8 | 71.8 | 37116 | 17 | US-10-107-431-279 | Sequence 279, App |
| c 34 | 15.8 | 71.8 | 109519 | 11 | US-09-758-759-1 | Sequence 1, Appli |
| c 35 | 15.6 | 70.9 | 25 | 21 | US-10-719-900-527126 | Sequence 527126, |
| c 36 | 15.6 | 70.9 | 118 | 20 | US-10-425-115-150443 | Sequence 150443, |
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| c 38 | 15.6 | 70.9 | 510 | 20 | US-10-425-115-125969 | Sequence 125969, |
| 39 | 15.6 | 70.9 | 624 | 20 | US-10-425-115-23654 | Sequence 23654, A |
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| c 41 | 15.6 | 70.9 | 690 | 20 | US-10-363-345A-11450 | Sequence 11450, A |
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| c 45 | 15.6 | 70.9 | 1358 | 18 | US-10-424-599-35716 | Sequence 35716, A |

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 10:06:45 ; Search time 173.874 Seconds
(without alignments)
4816.222 Million cell updates/sec

Title: US-10-074-246-25
Perfect score: 22
Sequence: 1 gccgtccagtcgttaatgtcgc 22

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Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| c | 4 | 17.2 | 78.2 | 402 | 7 | CO134696 | | CO134696 | EST829367 |
| c | 5 | 17.2 | 78.2 | 428 | 7 | CO137596 | | CO137596 | EST832267 |
| c | 6 | 17.2 | 78.2 | 557 | 8 | AZ396799 | | AZ396799 | 1M0161E03 |
| c | 7 | 17.2 | 78.2 | 664 | 9 | AG180620 | | AG180620 | Pan trogl |
| | 8 | 17.2 | 78.2 | 852 | 7 | CK416341 | | CK416341 | AUF_IpInt |
| | 9 | 17.2 | 78.2 | 879 | 8 | AQ271729 | | AQ271729 | nbxb0026J |

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| c | 10 | 17.2 | 78.2 | 949 | 9 | CNS070DV | AL423497 | T7 end of |
| | 11 | 17 | 77.3 | 894 | 9 | CNS03HB0 | AL244053 | Tetraodon |
| | 12 | 16.8 | 76.4 | 331 | 8 | AZ719254 | AZ719254 | RPCI-24-1 |
| c | 13 | 16.8 | 76.4 | 341 | 8 | AZ620126 | AZ620126 | 1M0452P10 |
| | 14 | 16.8 | 76.4 | 433 | 8 | AZ716289 | AZ716289 | RPCI-24-1 |
| | 15 | 16.8 | 76.4 | 547 | 8 | AZ901323 | AZ901323 | RPCI-24-1 |
| | 16 | 16.8 | 76.4 | 806 | 8 | AZ717730 | AZ717730 | RPCI-24-1 |
| c | 17 | 16.8 | 76.4 | 1350 | 9 | AG398251 | AG398251 | Mus muscu |
| c | 18 | 16.8 | 76.4 | 1649 | 9 | AG098046 | AG098046 | Pan trogl |
| c | 19 | 16.4 | 74.5 | 215 | 4 | BG349271 | BG349271 | 947030B12 |
| c | 20 | 16.4 | 74.5 | 363 | 4 | BG349270 | BG349270 | 947030B12 |
| c | 21 | 16.4 | 74.5 | 416 | 7 | CO524986 | CO524986 | 3530_1_16 |
| c | 22 | 16.4 | 74.5 | 431 | 4 | BI273510 | BI273510 | 949026E12 |
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| c | 24 | 16.4 | 74.5 | 472 | 6 | CB278998 | CB278998 | ru39d09.y |
| c | 25 | 16.4 | 74.5 | 515 | 4 | BM499183 | BM499183 | 947043D01 |
| c | 26 | 16.4 | 74.5 | 529 | 4 | BG360883 | BG360883 | 947043D01 |
| | 27 | 16.4 | 74.5 | 532 | 4 | BI319172 | BI319172 | 949026E12 |
| c | 28 | 16.4 | 74.5 | 536 | 9 | TA31E07Q | AL454323 | T. brucei |
| c | 29 | 16.4 | 74.5 | 552 | 6 | CA141332 | CA141332 | SCJFRT205 |
| c | 30 | 16.4 | 74.5 | 552 | 7 | CO534599 | CO534599 | 3530_1_22 |
| c | 31 | 16.4 | 74.5 | 555 | 4 | BI992275 | BI992275 | 1020058H0 |
| c | 32 | 16.4 | 74.5 | 624 | 8 | AQ651426 | AQ651426 | Sheared D |
| c | 33 | 16.4 | 74.5 | 917 | 3 | CNS09ENE | BX055062 | Single re |
| | 34 | 16.4 | 74.5 | 918 | 8 | AZ211507 | AZ211507 | SP_0155_B |
| c | 35 | 16.4 | 74.5 | 1025 | 7 | CF879123 | CF879123 | tric019xh |
| | 36 | 16.2 | 73.6 | 293 | 8 | AQ645354 | AQ645354 | RPCI93-Ec |
| c | 37 | 16.2 | 73.6 | 303 | 2 | BB498742 | BB498742 | BB498742 |
| c | 38 | 16.2 | 73.6 | 335 | 2 | AW969377 | AW969377 | EST381454 |
| c | 39 | 16.2 | 73.6 | 354 | 5 | BQ488000 | BQ488000 | 10-E8249- |
| c | 40 | 16.2 | 73.6 | 356 | 2 | BE614894 | BE614894 | 601280320 |
| | 41 | 16.2 | 73.6 | 357 | 8 | CC446822 | CC446822 | PUHBA36TD |
| c | 42 | 16.2 | 73.6 | 392 | 8 | AZ214685 | AZ214685 | Sheared D |
| c | 43 | 16.2 | 73.6 | 420 | 1 | AJ486483 | AJ486483 | AJ486483 |
| c | 44 | 16.2 | 73.6 | 441 | 4 | BJ472984 | BJ472984 | BJ472984 |
| | 45 | 16.2 | 73.6 | 450 | 7 | CO640664 | CO640664 | USDA-FP_1 |

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 07:50:25 ; Search time 164.059 Seconds
(without alignments)
7088.436 Million cell updates/sec

Title: US-10-074-246-48
Perfect score: 24
Sequence: 1 cggccgtccagtcgttaatgtcgc 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 24 | 100.0 | 323 | 6 | BD171699 | BD171699 Identific |
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| | 4 | 24 | 100.0 | 611 | 6 | BD171688 | BD171688 Identific |
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| | 6 | 24 | 100.0 | 628 | 6 | AX513137 | AX513137 Sequence |
| | 7 | 24 | 100.0 | 802 | 6 | AX513136 | AX513136 Sequence |
| | 8 | 24 | 100.0 | 110000 | 1 | AE000516_10 | Continuation (11 o |
| | 9 | 24 | 100.0 | 327650 | 1 | BX248337 | BX248337 Mycobacte |
| | 10 | 24 | 100.0 | 349306 | 1 | BX842575 | BX842575 Mycobacte |
| | 11 | 22 | 91.7 | 22 | 6 | BD171663 | BD171663 Identific |
| | 12 | 22 | 91.7 | 22 | 6 | AX278539 | AX278539 Sequence |
| | 13 | 22 | 91.7 | 22 | 6 | AX513096 | AX513096 Sequence |
| c | 14 | 19.2 | 80.0 | 300425 | 1 | AP005022 | AP005022 Streptomy |
| | 15 | 19 | 79.2 | 19 | 6 | AX513123 | AX513123 Sequence |
| c | 16 | 18.8 | 78.3 | 3276 | 6 | A44223 | A44223 Sequence 4 |
| c | 17 | 18.8 | 78.3 | 3276 | 6 | A72710 | A72710 Sequence 4 |
| c | 18 | 18.8 | 78.3 | 3276 | 6 | AR408850 | AR408850 Sequence |
| c | 19 | 18.8 | 78.3 | 3276 | 6 | AX002862 | AX002862 Sequence |
| c | 20 | 18.8 | 78.3 | 4314 | 8 | GLE18738 | Y18738 Gracilariop |
| c | 21 | 18.2 | 75.8 | 11533 | 1 | AE009124 | AE009124 Agrobacte |
| c | 22 | 18.2 | 75.8 | 12074 | 1 | AE008089 | AE008089 Agrobacte |
| c | 23 | 18.2 | 75.8 | 160042 | 2 | AL365211 | AL365211 Homo sapi |
| | 24 | 18.2 | 75.8 | 175968 | 9 | AC018684 | AC018684 Homo sapi |
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| c | 41 | 17.8 | 74.2 | 181497 | 9 | AC096670 | AC096670 Homo sapi |
| c | 42 | 17.8 | 74.2 | 214922 | 2 | AC150991 | AC150991 Bos tauru |
| c | 43 | 17.6 | 73.3 | 700 | 9 | HSA329475 | AJ329475 Homo sapi |
| | 44 | 17.6 | 73.3 | 959 | 3 | AF047615 | AF047615 Euroglyph |
| c | 45 | 17.6 | 73.3 | 1319 | 1 | ATIS426 | X56562 A.tumefacie |

Perfect score: 24
Sequence: 1 cggccgtccagtcgttaatgtcgc 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 4 | 24 | 100.0 | 648 | 8 | ABX10126 | Abx10126 M. tuberc |
| 5 | 24 | 100.0 | 648 | 8 | ABX10127 | Abx10127 M. bovis |
| 6 | 24 | 100.0 | 802 | 6 | ABS70084 | Abs70084 Mycobacte |
| 7 | 24 | 100.0 | 802 | 8 | ABX10110 | Abx10110 M. tuberc |
| 8 | 24 | 100.0 | 110000 | 4 | AAI99682_10 | Continuation (11 o |
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| 10 | 22 | 91.7 | 22 | 6 | ABS70044 | Abs70044 Mycobacte |
| 11 | 22 | 91.7 | 22 | 6 | ABA81861 | Aba81861 M tubercu |
| 12 | 22 | 91.7 | 22 | 8 | ABX10101 | Abx10101 M. tuberc |
| 13 | 19 | 79.2 | 19 | 6 | ABS70071 | Abs70071 Mycobacte |
| c 14 | 18.8 | 78.3 | 3276 | 2 | AAQ88050 | Aaq88050 Glucan Ly |
| c 15 | 18.8 | 78.3 | 3276 | 2 | AAQ87604 | Aaq87604 Fungus-in |
| c 16 | 18.8 | 78.3 | 3276 | 2 | AAV84193 | Aav84193 Gracilari |

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| | 17 | 18.2 | 75.8 | 229354 | 6 | ABQ74179 | Abq74179 Human cyt |
| c | 18 | 17.6 | 73.3 | 907 | 8 | ABZ52394 | Abz52394 Aspergill |
| c | 19 | 17.6 | 73.3 | 1989 | 3 | AAC64054 | Aac64054 Winter wh |
| c | 20 | 17.6 | 73.3 | 2006 | 2 | AAQ50147 | Aaq50147 Phospholi |
| c | 21 | 17.6 | 73.3 | 20000 | 9 | ADA00836 | Ada00836 Agrobacte |
| | 22 | 17.6 | 73.3 | 86248 | 10 | ADC00087 | Adc00087 Enterohae |
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| | 24 | 17.6 | 73.3 | 110000 | 4 | AAI99682_36 | Continuation (37 o |
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| c | 26 | 17.4 | 72.5 | 216 | 10 | ADE52337 | Ade52337 Norway ra |
| c | 27 | 17.4 | 72.5 | 216 | 10 | ADH56123 | Adh56123 Rat pain- |
| | 28 | 17.4 | 72.5 | 43011 | 12 | ADN01941 | Adn01941 Staphyloc |
| c | 29 | 17.2 | 71.7 | 1416 | 4 | ABL11553 | Abl11553 Drosophil |
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| c | 31 | 16.8 | 70.0 | 2383 | 5 | AAS89875 | Aas89875 DNA encod |
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| | 33 | 16.6 | 69.2 | 1425 | 5 | AAH68448 | Aah68448 C glutami |
| | 34 | 16.6 | 69.2 | 1554 | 4 | AAF71396 | Aaf71396 Corynebac |
| c | 35 | 16.6 | 69.2 | 2787 | 6 | ABK88156 | Abk88156 Alpha-iso |
| c | 36 | 16.6 | 69.2 | 5811 | 6 | ABK88159 | Abk88159 DNA encod |
| c | 37 | 16.6 | 69.2 | 5811 | 8 | ADA26477 | Ada26477 Alpha-iso |
| c | 38 | 16.6 | 69.2 | 6153 | 8 | ADA26478 | Ada26478 Alpha-iso |
| | 39 | 16.6 | 69.2 | 8446 | 6 | ADG79370 | Adg79370 Human sec |
| c | 40 | 16.6 | 69.2 | 11705 | 2 | AAV62160 | Aav62160 HSV-2 str |
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| | 42 | 16.6 | 69.2 | 37286 | 4 | AAS59522 | Aas59522 Propionib |
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| c | 44 | 16.6 | 69.2 | 85692 | 12 | ADI39159 | Adi39159 Streptomy |
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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 10:18:20 ; Search time 8.47584 Seconds
(without alignments)
4633.247 Million cell updates/sec

Title: US-10-074-246-48
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| c | 5 | 18.2 | 75.8 | 4800 | 4 US-09-902-540-562 | Sequence 562, App |
| | 6 | 18.2 | 75.8 | 229354 | 4 US-09-705-400-64 | Sequence 64, Appl |
| | 7 | 17.6 | 73.3 | 87563 | 3 US-09-453-702B-57 | Sequence 57, Appl |
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| | 9 | 17.2 | 71.7 | 26012 | 4 US-09-902-540-1212 | Sequence 1212, Ap |
| | 10 | 16.6 | 69.2 | 486 | 4 US-09-902-540-3038 | Sequence 3038, Ap |
| c | 11 | 16.6 | 69.2 | 1145 | 3 US-09-221-017B-944 | Sequence 944, App |
| | 12 | 16.6 | 69.2 | 1557 | 3 US-07-852-132A-12 | Sequence 12, Appl |

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| 13 | 16.6 | 69.2 | 1557 | 5 | PCT-US91-01327-12 | Sequence 12, Appl |
| 14 | 16.6 | 69.2 | 1557 | 6 | 5248670-2 | Patent No. 5248670 |
| 15 | 16.6 | 69.2 | 1557 | 6 | 5248670-2 | Patent No. 5248670 |
| 16 | 16.6 | 69.2 | 5105 | 4 | US-09-902-540-791 | Sequence 791, App |
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| c 23 | 16.2 | 67.5 | 2923 | 2 | US-07-989-847-7 | Sequence 7, Appli |
| c 24 | 16.2 | 67.5 | 2923 | 3 | US-08-469-411-7 | Sequence 7, Appli |
| c 25 | 16.2 | 67.5 | 2923 | 4 | US-09-780-601A-7 | Sequence 7, Appli |
| c 26 | 16.2 | 67.5 | 2923 | 6 | 5187076-5 | Patent No. 5187076 |
| c 27 | 16.2 | 67.5 | 2923 | 6 | 5187076-5 | Patent No. 5187076 |
| c 28 | 16.2 | 67.5 | 2943 | 4 | US-09-949-016-247 | Sequence 247, App |
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| c 42 | 16 | 66.7 | 2345 | 3 | US-09-512-650-1 | Sequence 1, Appli |
| c 43 | 16 | 66.7 | 2345 | 3 | US-09-480-142-1 | Sequence 1, Appli |
| c 44 | 16 | 66.7 | 2345 | 4 | US-09-573-555-2 | Sequence 2, Appli |
| c 45 | 16 | 66.7 | 3544 | 2 | US-08-485-139-3 | Sequence 3, Appli |

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 11:13:07 ; Search time 34.9145 Seconds
(without alignments)
4315.680 Million cell updates/sec

Title: US-10-074-246-48
Perfect score: 24
Sequence: 1 cggccgtccagtcgttaatgtcgc 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6330945 seqs, 3139162390 residues

Total number of hits satisfying chosen parameters: 12661890

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 24 | 100.0 | 802 | 14 | US-10-074-246-65 | Sequence 65, Appl | |
| 4 | 22 | 91.7 | 22 | 9 | US-09-817-014-72 | Sequence 72, Appl | |
| 5 | 22 | 91.7 | 22 | 14 | US-10-074-246-25 | Sequence 25, Appl | |
| 6 | 22 | 91.7 | 22 | 16 | US-10-056-229-72 | Sequence 72, Appl | |
| c 7 | 19.2 | 80.0 | 9025608 | 15 | US-10-156-761-1 | Sequence 1, Appli | |
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| c 11 | 18.8 | 78.3 | 3276 | 17 | US-10-448-139-4 | Sequence 4, Appli | |
| c 12 | 18.8 | 78.3 | 3276 | 21 | US-10-879-638-8 | Sequence 8, Appli | |
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| 15 | 17.6 | 73.3 | 2163 | 19 | US-10-437-963-15518 | Sequence 15518, A | |
| c 16 | 17.6 | 73.3 | 20000 | 10 | US-09-992-009-1 | Sequence 1, Appli | |
| 17 | 17.6 | 73.3 | 87563 | 14 | US-10-114-170-57 | Sequence 57, Appl | |
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| 24 | 16.6 | 69.2 | 1554 | 19 | US-10-781-014-73 | Sequence 73, Appl | |
| c 25 | 16.6 | 69.2 | 1554 | 20 | US-10-425-115-13416 | Sequence 13416, A | |
| c 26 | 16.6 | 69.2 | 2787 | 19 | US-10-466-085A-6 | Sequence 6, Appli | |
| c 27 | 16.6 | 69.2 | 5811 | 19 | US-10-466-085A-32 | Sequence 32, Appl | |
| c 28 | 16.6 | 69.2 | 85692 | 18 | US-10-461-194-1 | Sequence 1, Appli | |
| c 29 | 16.6 | 69.2 | 154746 | 10 | US-09-827-688-8 | Sequence 8, Appli | |
| c 30 | 16.6 | 69.2 | 3309400 | 9 | US-09-738-626-1 | Sequence 1, Appli | |
| 31 | 16.4 | 68.3 | 743 | 20 | US-10-425-115-173257 | Sequence 173257, | |
| c 32 | 16.2 | 67.5 | 25 | 21 | US-10-956-157-174238 | Sequence 174238, | |
| c 33 | 16.2 | 67.5 | 25 | 21 | US-10-956-157-216105 | Sequence 216105, | |
| c 34 | 16.2 | 67.5 | 397 | 17 | US-10-242-535A-33196 | Sequence 33196, A | |
| c 35 | 16.2 | 67.5 | 397 | 18 | US-10-085-783A-33196 | Sequence 33196, A | |
| c 36 | 16.2 | 67.5 | 408 | 20 | US-10-425-115-112345 | Sequence 112345, | |
| 37 | 16.2 | 67.5 | 472 | 21 | US-10-505-680-688 | Sequence 688, App | |
| c 38 | 16.2 | 67.5 | 600 | 21 | US-10-956-157-5912 | Sequence 5912, Ap | |
| c 39 | 16.2 | 67.5 | 2078 | 20 | US-10-425-115-51743 | Sequence 51743, A | |
| c 40 | 16.2 | 67.5 | 2085 | 20 | US-10-739-930-2710 | Sequence 2710, Ap | |
| c 41 | 16.2 | 67.5 | 2923 | 15 | US-10-101-510-7 | Sequence 7, Appli | |
| c 42 | 16.2 | 67.5 | 2923 | 17 | US-10-366-345-14 | Sequence 14, Appl | |
| c 43 | 16.2 | 67.5 | 2923 | 17 | US-10-375-150-7 | Sequence 7, Appli | |
| c 44 | 16.2 | 67.5 | 2943 | 21 | US-10-956-157-677 | Sequence 677, App | |
| 45 | 16.2 | 67.5 | 3133 | 17 | US-10-291-265-108 | Sequence 108, App | |

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 10:06:45 ; Search time 189.68 Seconds
(without alignments)
4816.222 Million cell updates/sec

Title: US-10-074-246-48
Perfect score: 24
Sequence: 1 cggccgtccagtcgtaatgtcgc 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
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6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | % Query Match | Length | DB | ID | Description |
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| c | 1 | 19.4 | 80.8 | 497 | 7 | CK101783 | CK101783 F118P27.5 |
| | 2 | 18.2 | 75.8 | 452 | 6 | CF026765 | CF026765 QCB11f12. |
| c | 3 | 18.2 | 75.8 | 664 | 9 | AG180620 | AG180620 Pan trogl |
| c | 4 | 18.2 | 75.8 | 949 | 9 | CNS070DV | AL423497 T7 end of |
| | 5 | 17.8 | 74.2 | 987 | 9 | CNS01U2J | AL167284 Tetraodon |
| c | 6 | 17.8 | 74.2 | 1143 | 9 | AG175746 | AG175746 Pan trogl |
| | 7 | 17.6 | 73.3 | 280 | 6 | CA081232 | CA081232 SCACAM204 |
| c | 8 | 17.6 | 73.3 | 314 | 8 | BH882141 | BH882141 hw35d05.b |

| | | | | | | | | |
|---|----|------|------|-----|---|----------|----------|-----------|
| c | 9 | 17.6 | 73.3 | 383 | 9 | CG229875 | CG229875 | OGWAK63TH |
| c | 10 | 17.6 | 73.3 | 402 | 7 | CO134696 | CO134696 | EST829367 |
| c | 11 | 17.6 | 73.3 | 424 | 8 | BZ774753 | BZ774753 | ii49b11.b |
| c | 12 | 17.6 | 73.3 | 428 | 7 | CO137596 | CO137596 | EST832267 |
| | 13 | 17.6 | 73.3 | 457 | 2 | BE516820 | BE516820 | WHE620_D0 |
| c | 14 | 17.6 | 73.3 | 540 | 4 | BJ214160 | BJ214160 | BJ214160 |
| c | 15 | 17.6 | 73.3 | 548 | 9 | CG272919 | CG272919 | OGWKC66TH |
| c | 16 | 17.6 | 73.3 | 600 | 8 | BZ619480 | BZ619480 | ig37a07.b |
| | 17 | 17.6 | 73.3 | 600 | 8 | BZ619481 | BZ619481 | ig37a07.g |
| c | 18 | 17.6 | 73.3 | 613 | 4 | BJ300459 | BJ300459 | BJ300459 |
| c | 19 | 17.6 | 73.3 | 630 | 4 | BJ244447 | BJ244447 | BJ244447 |
| c | 20 | 17.6 | 73.3 | 641 | 4 | BJ256609 | BJ256609 | BJ256609 |
| c | 21 | 17.6 | 73.3 | 650 | 8 | BH819001 | BH819001 | BACPP12-K |
| | 22 | 17.6 | 73.3 | 656 | 9 | CG824714 | CG824714 | SOYEB35TH |
| | 23 | 17.6 | 73.3 | 663 | 7 | CN132436 | CN132436 | OX1_6_D12 |
| | 24 | 17.6 | 73.3 | 695 | 9 | CL157668 | CL157668 | 104_345_1 |
| | 25 | 17.6 | 73.3 | 762 | 8 | BZ658927 | BZ658927 | OGCAZ20TC |
| | 26 | 17.6 | 73.3 | 775 | 7 | CN132518 | CN132518 | OX1_6_D12 |
| | 27 | 17.6 | 73.3 | 789 | 9 | CL686083 | CL686083 | PRI0143a_ |
| | 28 | 17.6 | 73.3 | 795 | 9 | CG214781 | CG214781 | OGXBK26TH |
| | 29 | 17.6 | 73.3 | 801 | 9 | CL666195 | CL666195 | PRI0151d_ |
| | 30 | 17.6 | 73.3 | 850 | 9 | CL654705 | CL654705 | PRI0121b_ |
| | 31 | 17.6 | 73.3 | 852 | 7 | CK416341 | CK416341 | AUF_IpInt |
| c | 32 | 17.6 | 73.3 | 864 | 8 | BZ658938 | BZ658938 | OGCAZ20TM |
| c | 33 | 17.6 | 73.3 | 880 | 6 | CD377821 | CD377821 | PTMM02990 |
| c | 34 | 17.6 | 73.3 | 893 | 6 | CD381395 | CD381395 | PTMM06564 |
| | 35 | 17.4 | 72.5 | 894 | 9 | CNS03HB0 | AL244053 | Tetraodon |
| c | 36 | 17.2 | 71.7 | 505 | 8 | BZ345288 | BZ345288 | hr48g03.b |
| | 37 | 17.2 | 71.7 | 512 | 4 | BI709947 | BI709947 | ft51d05.y |
| c | 38 | 17.2 | 71.7 | 513 | 8 | BZ345049 | BZ345049 | hr44a11.b |
| | 39 | 17.2 | 71.7 | 548 | 7 | CK351188 | CK351188 | hggfha34D |
| c | 40 | 17.2 | 71.7 | 557 | 8 | AZ396799 | AZ396799 | 1M0161E03 |
| c | 41 | 17.2 | 71.7 | 583 | 7 | CO661192 | CO661192 | DG31-190g |
| c | 42 | 17.2 | 71.7 | 649 | 1 | AI297657 | AI297657 | LP12009.5 |
| c | 43 | 17.2 | 71.7 | 651 | 1 | AI260496 | AI260496 | LP04383.5 |
| c | 44 | 17.2 | 71.7 | 660 | 7 | CR369078 | CR369078 | CR369078 |
| c | 45 | 17.2 | 71.7 | 667 | 4 | BI588806 | BI588806 | RH30239.5 |

Title: US-10-074-246-52
 Perfect score: 19
 Sequence: 1 ccggtccagtcggttaatgtc 19

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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 2: gb_htg:*
 3: gb_in:*
 4: gb_om:*
 5: gb_ov:*
 6: gb_pat:*
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 8: gb_pl:*
 9: gb_pr:*
 10: gb_ro:*
 11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
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| 2 | 19 | 100.0 | 22 | 6 | BD171663 | BD171663 Identific |
| 3 | 19 | 100.0 | 22 | 6 | AX278539 | AX278539 Sequence |
| 4 | 19 | 100.0 | 22 | 6 | AX513096 | AX513096 Sequence |
| 5 | 19 | 100.0 | 24 | 6 | AX513119 | AX513119 Sequence |
| 6 | 19 | 100.0 | 323 | 6 | BD171699 | BD171699 Identific |
| 7 | 19 | 100.0 | 369 | 6 | BD171700 | BD171700 Identific |
| 8 | 19 | 100.0 | 611 | 6 | BD171688 | BD171688 Identific |
| 9 | 19 | 100.0 | 611 | 6 | BD171689 | BD171689 Identific |
| 10 | 19 | 100.0 | 628 | 6 | AX513137 | AX513137 Sequence |
| 11 | 19 | 100.0 | 802 | 6 | AX513136 | AX513136 Sequence |
| 12 | 19 | 100.0 | 110000 | 1 | AE000516_10 | Continuation (11 o |
| 13 | 19 | 100.0 | 327650 | 1 | BX248337 | BX248337 Mycobacte |
| 14 | 19 | 100.0 | 349306 | 1 | BX842575 | BX842575 Mycobacte |

| | | | | | | | |
|---|----|------|------|--------|----|-----------|--------------------|
| c | 15 | 17.4 | 91.6 | 214922 | 2 | AC150991 | AC150991 Bos tauru |
| c | 16 | 16.4 | 86.3 | 174913 | 3 | AY613856 | AY613856 Oikopleur |
| | 17 | 16 | 84.2 | 203592 | 10 | AL669921 | AL669921 Mouse DNA |
| | 18 | 15.8 | 83.2 | 620 | 10 | MUSMHW282 | M16240 Mouse MHC c |
| c | 19 | 15.8 | 83.2 | 1145 | 6 | AR227484 | AR227484 Sequence |
| | 20 | 15.8 | 83.2 | 1362 | 6 | AX078488 | AX078488 Sequence |
| c | 21 | 15.8 | 83.2 | 3276 | 6 | A44223 | A44223 Sequence 4 |
| c | 22 | 15.8 | 83.2 | 3276 | 6 | A72710 | A72710 Sequence 4 |
| c | 23 | 15.8 | 83.2 | 3276 | 6 | AR408850 | AR408850 Sequence |
| c | 24 | 15.8 | 83.2 | 3276 | 6 | AX002862 | AX002862 Sequence |
| c | 25 | 15.8 | 83.2 | 3646 | 1 | AY318856 | AY318856 Acetobact |
| | 26 | 15.8 | 83.2 | 3849 | 6 | AR385744 | AR385744 Sequence |
| c | 27 | 15.8 | 83.2 | 4314 | 8 | GLE18738 | Y18738 Gracilariop |
| c | 28 | 15.8 | 83.2 | 11135 | 1 | AE011096 | AE011096 Methanosa |
| c | 29 | 15.8 | 83.2 | 20389 | 1 | AE008768 | AE008768 Salmonell |
| | 30 | 15.8 | 83.2 | 70290 | 2 | AC100833 | AC100833 Homo sapi |
| | 31 | 15.8 | 83.2 | 71239 | 2 | AC099903 | AC099903 Mus muscu |
| c | 32 | 15.8 | 83.2 | 71239 | 2 | AC099903 | AC099903 Mus muscu |
| c | 33 | 15.8 | 83.2 | 115857 | 8 | AC147407 | AC147407 Medicago |
| | 34 | 15.8 | 83.2 | 144301 | 9 | AC010467 | AC010467 Homo sapi |
| c | 35 | 15.8 | 83.2 | 150010 | 9 | AC104782 | AC104782 Homo sapi |
| c | 36 | 15.8 | 83.2 | 155164 | 9 | AC005165 | AC005165 Homo sapi |
| c | 37 | 15.8 | 83.2 | 155666 | 10 | AC134830 | AC134830 Mus muscu |
| | 38 | 15.8 | 83.2 | 155862 | 9 | AC018464 | AC018464 Homo sapi |
| | 39 | 15.8 | 83.2 | 159681 | 10 | AC132088 | AC132088 Mus muscu |
| c | 40 | 15.8 | 83.2 | 160042 | 2 | AL365211 | AL365211 Homo sapi |
| | 41 | 15.8 | 83.2 | 162167 | 2 | AC019271 | AC019271 Homo sapi |
| c | 42 | 15.8 | 83.2 | 162167 | 2 | AC019271 | AC019271 Homo sapi |
| c | 43 | 15.8 | 83.2 | 169393 | 9 | AC146016 | AC146016 Pan trogl |
| c | 44 | 15.8 | 83.2 | 173719 | 5 | BX005313 | BX005313 Zebrafish |
| | 45 | 15.8 | 83.2 | 174217 | 2 | AC021408 | AC021408 Homo sapi |

ALIGNMENTS

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 07:50:25 ; Search time 22.7553 Seconds
(without alignments)
4942.816 Million cell updates/sec

Title: US-10-074-246-52
Perfect score: 19
Sequence: 1 ccgtccagtcgттаатgтc 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: geneseqn2002bs:*
8: geneseqn2003as:*
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10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 19 | 100.0 | 22 | 6 | ABS70044 | Abs70044 Mycobacte | |
| 3 | 19 | 100.0 | 22 | 6 | ABA81861 | Aba81861 M. tubercu | |
| 4 | 19 | 100.0 | 22 | 8 | ABX10101 | Abx10101 M. tuberc | |
| 5 | 19 | 100.0 | 24 | 6 | ABS70067 | Abs70067 Mycobacte | |

| | | | | | | | |
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| | 6 | 19 | 100.0 | 628 | 6 | ABS70085 | Abs70085 Mycobacte |
| | 7 | 19 | 100.0 | 628 | 8 | ABX10111 | Abx10111 M. bovis |
| | 8 | 19 | 100.0 | 648 | 8 | ABX10126 | Abx10126 M. tuberc |
| | 9 | 19 | 100.0 | 648 | 8 | ABX10127 | Abx10127 M. bovis |
| | 10 | 19 | 100.0 | 802 | 6 | ABS70084 | Abs70084 Mycobacte |
| | 11 | 19 | 100.0 | 802 | 8 | ABX10110 | Abx10110 M. tuberc |
| | 12 | 19 | 100.0 | 110000 | 4 | AAI99682_10 | Continuation (11 o |
| | 13 | 19 | 100.0 | 110000 | 4 | AAI99683_10 | Continuation (11 o |
| c | 14 | 15.8 | 83.2 | 417 | 8 | ABZ52746 | Abz52746 Aspergill |
| | 15 | 15.8 | 83.2 | 1362 | 4 | AAF60956 | Aaf60956 P. putida |
| c | 16 | 15.8 | 83.2 | 3276 | 2 | AAQ88050 | Aaq88050 Glucan Ly |
| c | 17 | 15.8 | 83.2 | 3276 | 2 | AAQ87604 | Aaq87604 Fungus-in |
| c | 18 | 15.8 | 83.2 | 3276 | 2 | AAV84193 | Aav84193 Gracilari |
| | 19 | 15.8 | 83.2 | 3738 | 8 | ACA36064 | Aca36064 Prokaryot |
| | 20 | 15.8 | 83.2 | 3849 | 11 | ACH96678 | Ach96678 Klebsiell |
| c | 21 | 15.8 | 83.2 | 4316 | 10 | ADB69197 | Adb69197 C. neofor |
| | 22 | 15.8 | 83.2 | 229354 | 6 | ABQ74179 | Abq74179 Human cyt |
| | 23 | 15.4 | 81.1 | 1157 | 3 | AAF11578 | Aaf11578 Aspergill |
| c | 24 | 15.4 | 81.1 | 2383 | 5 | AAS89875 | Aas89875 DNA encod |
| c | 25 | 15.4 | 81.1 | 2451 | 5 | AAS85748 | Aas85748 DNA encod |
| | 26 | 15.4 | 81.1 | 28136 | 4 | AAK69755 | Aak69755 Human imm |
| | 27 | 15.4 | 81.1 | 43011 | 12 | ADN01941 | Adn01941 Staphyloc |
| | 28 | 14.8 | 77.9 | 23 | 12 | ADM94964 | Adm94964 Herpes si |
| c | 29 | 14.8 | 77.9 | 439 | 6 | ABN96003 | Abn96003 Gene #250 |
| | 30 | 14.8 | 77.9 | 549 | 3 | AAC95228 | Aac95228 Cat flea |
| c | 31 | 14.8 | 77.9 | 617 | 3 | AAF08207 | Aaf08207 Fusarium |
| c | 32 | 14.8 | 77.9 | 716 | 3 | AAA54328 | Aaa54328 Sequence |
| c | 33 | 14.8 | 77.9 | 725 | 12 | ADQ17340 | Adq17340 Human sof |
| c | 34 | 14.8 | 77.9 | 792 | 12 | ADL12782 | Adl12782 Human ste |
| c | 35 | 14.8 | 77.9 | 927 | 2 | AAT51317 | Aat51317 HSV glyco |
| | 36 | 14.8 | 77.9 | 930 | 4 | AAH33866 | Aah33866 Human col |
| c | 37 | 14.8 | 77.9 | 1044 | 10 | ABZ66697 | Abz66697 Orthosomy |
| | 38 | 14.8 | 77.9 | 1086 | 12 | ADO48504 | Ado48504 Human 108 |
| | 39 | 14.8 | 77.9 | 1140 | 6 | ABQ22020 | Abq22020 Oligonucl |
| c | 40 | 14.8 | 77.9 | 1140 | 6 | ABQ22021 | Abq22021 Oligonucl |
| c | 41 | 14.8 | 77.9 | 1170 | 13 | ADT42664 | Adt42664 Bacterial |
| c | 42 | 14.8 | 77.9 | 1180 | 2 | AAZ10960 | Aaz10960 HSV-2 gly |
| c | 43 | 14.8 | 77.9 | 1185 | 2 | AAZ10959 | Aaz10959 HSV-1 gly |
| c | 44 | 14.8 | 77.9 | 1185 | 10 | ADF12414 | Adf12414 Herpes si |
| c | 45 | 14.8 | 77.9 | 1185 | 12 | ADG39432 | Adg39432 HSV glyco |

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 10:18:20 ; Search time 6.71004 Seconds
(without alignments)
4633.247 Million cell updates/sec

Title: US-10-074-246-52
Perfect score: 19
Sequence: 1 ccgtccagtcgттаатgтc 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | | % | | | | ID | Description |
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| | 2 | 19 | 100.0 | 4411529 | 3 | US-09-103-840A-1 | | Sequence 1, Appli |
| C | 3 | 15.8 | 83.2 | 1145 | 3 | US-09-221-017B-944 | | Sequence 944, App |
| C | 4 | 15.8 | 83.2 | 1305 | 4 | US-09-902-540-4277 | | Sequence 4277, Ap |
| C | 5 | 15.8 | 83.2 | 3276 | 3 | US-08-633-768A-4 | | Sequence 4, Appli |
| C | 6 | 15.8 | 83.2 | 3276 | 4 | US-09-280-197-4 | | Sequence 4, Appli |
| | 7 | 15.8 | 83.2 | 3849 | 4 | US-09-489-039A-2473 | | Sequence 2473, Ap |
| | 8 | 15.8 | 83.2 | 26012 | 4 | US-09-902-540-1212 | | Sequence 1212, Ap |
| | 9 | 15.8 | 83.2 | 229354 | 4 | US-09-705-400-64 | | Sequence 64, Appl |
| C | 10 | 15 | 78.9 | 765 | 4 | US-09-248-796A-1849 | | Sequence 1849, Ap |
| | 11 | 14.8 | 77.9 | 601 | 4 | US-09-949-016-206008 | | Sequence 206008, |

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| | 12 | 14.8 | 77.9 | 601 | 4 | US-09-949-016-206009 | Sequence 206009, |
| c | 13 | 14.8 | 77.9 | 792 | 4 | US-09-976-594-511 | Sequence 511, App |
| c | 14 | 14.8 | 77.9 | 927 | 1 | US-08-499-568-1 | Sequence 1, Appli |
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| c | 16 | 14.8 | 77.9 | 1180 | 4 | US-09-247-890-2 | Sequence 2, Appli |
| c | 17 | 14.8 | 77.9 | 1180 | 4 | US-09-724-969-2 | Sequence 2, Appli |
| c | 18 | 14.8 | 77.9 | 1180 | 4 | US-09-724-852-2 | Sequence 2, Appli |
| c | 19 | 14.8 | 77.9 | 1185 | 4 | US-09-247-890-1 | Sequence 1, Appli |
| c | 20 | 14.8 | 77.9 | 1185 | 4 | US-09-724-969-1 | Sequence 1, Appli |
| c | 21 | 14.8 | 77.9 | 1185 | 4 | US-09-724-852-1 | Sequence 1, Appli |
| c | 22 | 14.8 | 77.9 | 1204 | 1 | US-07-829-947A-1 | Sequence 1, Appli |
| c | 23 | 14.8 | 77.9 | 1204 | 5 | PCT-US93-00945-1 | Sequence 1, Appli |
| c | 24 | 14.8 | 77.9 | 1242 | 4 | US-09-247-890-3 | Sequence 3, Appli |
| c | 25 | 14.8 | 77.9 | 1242 | 4 | US-09-724-969-3 | Sequence 3, Appli |
| c | 26 | 14.8 | 77.9 | 1242 | 4 | US-09-724-852-3 | Sequence 3, Appli |
| c | 27 | 14.8 | 77.9 | 1459 | 6 | 5182195-9 | Patent No. 5182195 |
| c | 28 | 14.8 | 77.9 | 1459 | 6 | 5182195-9 | Patent No. 5182195 |
| c | 29 | 14.8 | 77.9 | 1550 | 1 | US-08-499-568-10 | Sequence 10, Appl |
| c | 30 | 14.8 | 77.9 | 1550 | 1 | US-08-793-958-10 | Sequence 10, Appl |
| c | 31 | 14.8 | 77.9 | 1608 | 1 | US-08-499-568-3 | Sequence 3, Appli |
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| c | 33 | 14.8 | 77.9 | 1635 | 1 | US-08-499-568-14 | Sequence 14, Appl |
| c | 34 | 14.8 | 77.9 | 1635 | 1 | US-08-793-958-14 | Sequence 14, Appl |
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| | 45 | 14.4 | 75.8 | 2526 | 4 | US-09-252-991A-10348 | Sequence 10348, A |

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 11:13:07 ; Search time 27.6406 Seconds
(without alignments)
4315.680 Million cell updates/sec

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Perfect score: 19
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6330945 seqs, 3139162390 residues

Total number of hits satisfying chosen parameters: 12661890

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 19 | 100.0 | 22 | 9 | US-09-817-014-72 | Sequence 72, Appl | |
| 3 | 19 | 100.0 | 22 | 14 | US-10-074-246-25 | Sequence 25, Appl | |
| 4 | 19 | 100.0 | 22 | 16 | US-10-056-229-72 | Sequence 72, Appl | |
| 5 | 19 | 100.0 | 24 | 14 | US-10-074-246-48 | Sequence 48, Appl | |
| 6 | 19 | 100.0 | 628 | 14 | US-10-074-246-66 | Sequence 66, Appl | |
| 7 | 19 | 100.0 | 802 | 14 | US-10-074-246-65 | Sequence 65, Appl | |
| 8 | 16.4 | 86.3 | 743 | 20 | US-10-425-115-173257 | Sequence 173257, | |
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| 14 | 15.8 | 83.2 | 3738 | 17 | US-10-282-122A-23934 | Sequence 23934, A | |
| c 15 | 15.8 | 83.2 | 4316 | 17 | US-10-320-797-324 | Sequence 324, App | |
| 16 | 15.8 | 83.2 | 218802 | 21 | US-10-897-508-1 | Sequence 1, Appli | |
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| 18 | 15.4 | 81.1 | 1157 | 20 | US-10-653-047-4101 | Sequence 4101, Ap | |
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| 20 | 14.8 | 77.9 | 23 | 16 | US-10-165-410A-16 | Sequence 16, Appl | |
| 21 | 14.8 | 77.9 | 25 | 21 | US-10-719-900-182550 | Sequence 182550, | |
| c 22 | 14.8 | 77.9 | 263 | 20 | US-10-425-115-165317 | Sequence 165317, | |
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| c 32 | 14.8 | 77.9 | 930 | 15 | US-10-106-698-932 | Sequence 932, App | |
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| c 42 | 14.8 | 77.9 | 1180 | 9 | US-09-247-890-2 | Sequence 2, Appli | |
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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 10:06:45 ; Search time 150.164 Seconds
(without alignments)
4816.222 Million cell updates/sec

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Perfect score: 19
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| c | 7 | 16.4 | 86.3 | 529 | 4 | BG360883 | BG360883 947043D01 |
| | 8 | 16.4 | 86.3 | 532 | 4 | BI319172 | BI319172 949026E12 |
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| c | 11 | 16.4 | 86.3 | 555 | 4 | BI992275 | BI992275 1020058H0 |
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| c | 43 | 15.4 | 81.1 | 491 | 4 | BM344145 | BM344145 rr47c11.y |
| | 44 | 15.4 | 81.1 | 496 | 5 | BU052092 | BU052092 gd47f06.y |
| | 45 | 15.4 | 81.1 | 510 | 9 | CL336275 | CL336275 RPCI44_25 |

D-103.**A Prospective Comparison of the MB/BacT™ and Conventional Culturing in a High-Volume Clinical Mycobacteriology Laboratory.**

L. STOCKMAN,* D. R. MILLER, and G.D. ROBERTS, Mayo Clinic and Mayo Foundation, Rochester, MN.

During the last decade, with the pressures of managed care, emphasis has been placed on rapid turn-around time, efficient use of technical personnel, and generation of accurate results to aid in patient care. The purpose of this study was to validate the MB/BacT™ instrument and the BacT/View software in a high volume mycobacteriology laboratory. To date, 1105 specimens have been decontaminated and 0.5 mL cultured to BACTEC® 12B Mycobacteria culture vials (BAC), 7H10 and 7H11S (SOL), and MB/BacT™ Process Bottles (MB/B). SOL were read weekly for 8 weeks. BAC were read twice a week for 3 weeks and weekly for 3 weeks, any bottle with a GI = 10 was considered positive and aliquots were placed onto a Blood agar (BAP) and into a cytospin AF (Acid fast stain). The MB/B was automatically monitored every 10 min for 6 weeks and positive bottles analyzed by culture (BAP) and smear (AF). All AFB (acid fast bacilli) were identified by probes, biochemicals and/or gas liquid chromatography. Of the 465 cultures completed, 98 cultures were positive and identification of 11 is pending. Isolates recovered include: 50 *M. avium intracellulare* complex (MAI), 2 *M. chelonae* (CHEL), 17 *M. gordonae* (GO) and 16 *M. tuberculosis* complex (TB). 2 cultures had MAI and CHEL, and MAI and GO, respectively. 57 were positive for AFB in BAC and MB/B. 13 were positive in MB/B only. 6 were positive in BAC only. Of 39 MAI positive in both systems, BAC had an average detection of 7.2 d and range 2-28 d, MB/B had an average 14.5 d and range 2.6-40.7 d. Of the 14 TB positive in both systems, BAC had an average day to detection 9.5 d, and range 8.4-28 d, MB/B had an average 15.8 d, and range 8.5-28.2 d. Due to the instrumentation and BACT/View software, the MB/B was easier to use and required less "hands-on" time. These preliminary results, however, suggest that the MB/B requires a longer incubation time to detection.

D-104.**P34 and F57 Based-Multiplex PCR Assay for Discrimination between Tuberculous and Nontuberculous Mycobacteria.**

P. VANNUFFEL, C. COETSIER, M. BOUYER, M. PHILIPPE, J.L. GALA, Queen Astrid Military Hosp. and Univ. of Louvain Medical School, Brussels, Belgium.

The nucleotide sequences, 5' to the open reading frame encoding the 34 kDa mycobacterial antigenic protein P34, were sequenced in both tuberculous (*M. tuberculosis* and *M. bovis*) (MTB) and non-tuberculous (*M. avium* and *M. paratuberculosis*) (MAC) mycobacteria. Multiple sequences alignment of this non-transcribed region (5'-NTR) revealed interspecies polymorphisms characterizing both mycobacterial groups: 5'-NTR in MTB species was 79 bases shorter compared to MAC. Conversely, 5'-NTR appeared to be highly conserved within each group: species differentiation relied on a single T to C transition for *M. tuberculosis* and *M. bovis*, and a single C to G transversion for *M. avium* and *M. paratuberculosis*. In a first step, a polymerase chain reaction (PCR) assay discriminating MTB from MAC complexes was developed. Primers matching conserved sequences bordering the polymorphic 5'-NTR amplified a 178 bp fragment in MTB and a 257 bp fragment in MAC, irrespective of the species. In a next step, amplification of a 420 bp product from the genomic sequence P57 (1) allowed a specific identification of *M. paratuberculosis* within the MAC group, and was therefore co-amplified with P34. Based on the P34 and F57 multiplex assay, a distinct amplification pattern was obtained for three of the four mycobacteria: *M. paratuberculosis* was characterized by the presence of the 420 bp and 257 bp fragments, *M. avium* by the 257 bp fragment only, while *M. tuberculosis* and *M. bovis* indistinctly produced a 178 bp amplicon. Finally, the specificity

of the multiplex assay was confirmed, for the four species, by using a wide panel of reference mycobacteria (n=10), including *M. intracellulare*, *M. africanum*, *M. microti*, *M. scrofulaceum*, *M. kansasii* and *M. gordonae*, and a larger collection of clinical specimens (n=30). While coincidentally also applicable in veterinary medicine, P34 and F57 multiplex assay appears relevant for the detection of human tuberculosis and opportunistic *M. avium* infections in AIDS patients, and can also be used to assess the putative role of *M. paratuberculosis* in Crohn's disease or sarcoidosis.

D-105.**Evaluation of the BBL MGIT™ AST SIRE System for Susceptibility Testing of *M. tuberculosis*.**

B.A. HANNA, C.H. REXER, S.B. WALTERS, NYU School of Medicine, Bellevue Hosp. New York, NY.

The global incidence of multidrug-resistant tuberculosis (MDRTB) emphasizes the need for a simple and reliable method for susceptibility testing of *Mycobacterium tuberculosis* (Mtb). We compared the Mycobacteria Growth Indicator Tube Antimycobacterial Susceptibility Test system (MGIT™AST, Becton Dickinson) to the method of proportion (MOP) disk elution method for the antimycobacterial susceptibility testing of Mtb. The MGIT AST is a four drug rapid susceptibility test system with critical concentrations (µg/ml) of Streptomycin (STR) - 0.8, Isoniazid (INH) - 0.1, Rifampin (RIF) - 1.0 and Ethambutol (EMB) - 3.5, in individual MGIT culture tubes containing modified Middlebrook 7H9 broth and MGIT OADC enrichment along with a growth control tube. For comparison, critical concentrations (µg/ml) tested by MOP were INH - 0.2 and 1.0, RIF - 1.0, STR - 2.0 and 10.0 and EMB - 5.0. For the study, 40 clinical isolates of Mtb including 8 MDRTB, were inoculated to the MGIT AST system and monitored daily for growth. Each isolate was tested in pairs using both a liquid medium (MGIT) and a solid medium (L-J) as the inoculum source. Tubes were read daily, and all growth control tubes were noted to be positive within 3-5 days. Results for drug containing tubes were interpreted when growth was first noted, or within 2 days of the growth control becoming positive. Among the 320 "bug-drug" comparisons there were 5 discordant results: INH: none discordant; RIF: 1 isolate was MGIT R but MOP S in one of the paired tests; STR: 1 isolate was MGIT S but MOP R in one of the paired tests; EMB: 1 isolate was MGIT R but MOP S in one pair, a second isolate was MGIT R but MOP S in both pairs. The MGIT AST is a simple to use, rapid test to detect MDRTB, with excellent comparability to the conventional MOP.

D-106.**rpoB Mutations in *Mycobacterium tuberculosis* (MTB): an Analysis Using the Polymerase Chain Reaction and Single-Stranded Conformational Polymorphism (PCR-SSCP).**

M. BOBADILLA, A. PONCE-DE-LEON*, C. ARENAS, P. COUARY, A. MARTINEZ, G.M. RUIZ-PALACIOS, and J. SIFUENTES-OSORNIO, Inst. Natl. De La Nutricion Salvador Zubiran, Mexico City, Mexico.

Introduction: Resistance to antituberculous agents is an alarming public health problem. A rapid amplification method has been developed that uses SSCP to identify mutations that codify for rifampin (RIF) resistance, which is associated to multi-drug resistance. **Objective:** To determine mutations in the *rpoB* gene of MTB clinical isolates with different levels of resistance to RIF using PCR-SSCP analysis. **Methods:** 45 distinct clinical isolates resistant to at least one antituberculous agent were fully characterized by conventional methods. Minimal inhibitory concentrations (MICs) to RIF were determined by the radiometric method (BACTEC 460, Becton Dickinson, Mexico). DNA was extracted using conventional methods. PCR conditions: 10 pM of TB8 (5'TGCACGTCGCGGACCTCCA 3') and TB9 (5'TCGCGCGCATCAAGGAGT 3') primers (coding for a 157-bp stretch